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RESULT 2
BD249810 2774 bp DNA linear PAT 17-JUL-2003

LOCUS BD249810 33 human secreted proteins.
DEFINITION BD249810
ACCESSION BD249810.1 GI:33059580
VERSION JP 2002540763-A/12.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 2774)
Rosen,C.A., Ruben,S.M., Ebner,R., Young,P.B., Ni,J., Soppet,D.R.,
Moore,P.A., Shi,Y., Lafleur,D.W., Olsen,H.S., Florence,K.A. and
Komatsoulis,G.

REFERENCE 33 human secreted proteins
AUTHORS Patent: JP 2002540763-A 12 03-DEC-2002;
JOURNAL HUMAN GENOME SCIENCES INC
TITLE OS Homo sapiens (human)
COMMENT PN JP 2002540763-A/12
PD 03-DEC-2002
PR 08-FEB-2000 JP 2000598519
PI 10-FEB-1999 US 60/119468
PI CRAIG A ROSEN, STEVEN M RUBEN, REINHARD EBNER, PAUL E YOUNG, JIAN
PI NI, DANIEL R SOPPET, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR, HENRIK

PI S OLSEN,
PI KIMBERLY A FLORENCE, GEORGE KOMATSOLIS
PC C12N15/09, A61K31/7115, A61K38/00, A61K48/00, A61P1/00, A61P1/04,
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ORIGIN

Query Match 96.8%; Score 2617.2; DB 6; Length 2774;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2669; Conservative 6; Mismatches 22; Indels 7; Gaps 4;

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QY 421 ACCTGTCMAAGCTTAAGTCAACATGGGTCTGAGAGCAATGAATGCAACCTGTGTGA 480
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Db	2170	ACTMAGATCAAAATTTGTGTGAGCGGTGGTGGTGGACCTGTATTTCCAGCTACTG		2229
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Db	2230	GAGGCCAAGCATGAGATCGCTTGAACCTGGAGGTGAGTGAAGTGAAGTGAAGTGAATG		2289
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Oy	2697	AAAAA 2700		
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LOCUS	AB027233	Homo sapiens mRNA for membrane protein FOAP-12, complete cds.		
DEFINITION	AB027233.1	GI:14517605		
ACCESSION	AB027233	membrane protein FOAP-12.		
VERSION	AB027233.1	GI:14517605		
KEYWORDS	membrane protein FOAP-12.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Memakia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Fujii,Y., Takayama,K., Teuriltani,K., Yajima,Y., Amemiya,T., Urai,Y., Naito,K. and Kawaguchi,A.			
TITLE	Homo sapiens mRNA for FOAP-12 protein, complete cds			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 2672)			
AUTHORS	Fujii,Y., Takayama,K., Teuriltani,K., Yajima,Y., Amemiya,T.,			

TITLE

Ukai, Y., Naito, K. and Kawaguchi, A.

JOURNAL

Submitted (12-MAY-1999) Yasuyuki Fujii, Taisho Pharmaceutical Co., Ltd., Molecular Biology Laboratory, Yoshino-cho, 1-403, Ohmura, Saitama 3308530, Japan (E-mail: s7561@cm.taisho.co.jp, Tel: +81-48-663-1111, Fax: +81-48-652-7254)

Location/Qualifiers

FEATURES

source

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ORIGIN

Query Match 96.3%; Score 2604.6; DB 9; Length 2672;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 2658; Conservative 0; Mismatches 9; Indels 8; Gaps 4;

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Db 1081 AAAACATCAGAAATTCATGATTTGATGAAATCATAAGAAATGAAGATGTT 1140

Qy 1167 GACTTTTTCAGAGATTAATCTGTATGCTTCTTAAGATTAAGATGTTATTC 1226

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KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

REMARK
COMMENT

FEATURES

gene

MGC.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2658)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Shauler,G.D., Altschul,S.P., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bat.N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Spatcheon,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mulhany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettaman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzyzinski,M.I., Skalski,U., Snailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A. Human generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
2 (bases 1 to 2658)
12477932
Strausberg,R.
Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2530, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC).
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@hgrl.nih.gov
Akheri,N., Ayale,C., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granitz,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Khong,P., Laric,P., Legaspi,R., Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stentriop,S., Thomas,P.J., Touchman,J.W., Tsurgoum,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAX File: 49 Row: e Column: 22
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ORIGIN

Query Match 88.4%; Score 2390.6; DB 9; Length 2658;
 Best Local Similarity 95.5%; Pred. No. 0;
 Matches 2558; Conservative 0; Mismatches 9; Indels 112; Gaps 5;

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VERSION AL834424.1 GI:21740141
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REFERENCE 1 (bases 1 to 2445)
Bloecker, H., Boecher, M., Brandt, P., Newes, H. W., Weill, B. and Wiemann, S.
AUTHORS
TITLE Direct Submission

JOURNAL
COMMENT
Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
Sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp667F126) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at <http://mips.gsf.de/proj/cDNA/>.
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33 human secreted proteins
Patent: JP 2002540763-A 43 03-DEC-2002;
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PN JP 2002540763-A/43
PD 03-DEC-2002
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PR 10-FEB-1999 US 60/119468
PI CRAIG A ROSEN, STEVEN M RUBEN, REINHARD BEHNER, PAUL E YOUNG, JIAN
PI NI
PI DANIEL R SOPPET, PAUL A MOORE, YANGGU SHI, DAVID W IAFLEUR, HENRIK
PI S OLSEN,
PI KIMBERLY A FLORENCE, GEORGE KOMATSOULIS
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COMMENT

On Mar 1, 2001 this sequence version replaced gi:11878529.
----- Genome Center
Center: Stanford DNA Sequencing and Technology Development
Center
Center code: SBDTC
Web site: <http://sequence-www.stanford.edu/group/human/>
Contact: hum-info@sequence.stanford.edu

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----- Project Information
Center Project name: 922
Center Clone name: RP11-8D14
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Assembly program: Phrap; version 0.990319
Consensus quality: 160988 bases at least Q40
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Consensus quality: 161956 bases at least Q20
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Insert size: 165945; sum-of-contigs
Quality coverage: 9.0x in Q20 bases; agarose-fp
Quality coverage: 8.9x in Q20 bases; sum-of-contigs.
NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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 LOCUS
 DEFINITION Human DNA sequence from clone RP11-404F10 on chromosome 1q23.1-24.1. Contains the 5' end of the SLAM gene for signaling lymphocytic activation molecule, a SET (SET translocation (myeloid leukemia-associated)) protein pseudogene, the CD48 gene for CD48 antigen (B-cell membrane protein), the gene for a novel LY9 (lymphocyte antigen 9) like protein and the 5' end of the LY9 gene. Contains ESTs, STS and GSSs, complete sequence.
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 1 (bases 1 to 195976)
 BATES,K.
 Direct Submission
 Submitted (04-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SH, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 On Mar 6, 2000 this sequence version replaced gi:6983370.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormep
 This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at

FEATURES
 source
 http://www.sanger.ac.uk/HGP/Chr1
 RP11-404F10 is from the library RPCT-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
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AUTHORS Rosen, C.A., Ruben, S.M., Ebner, R., Young, P.E., Ni, U., Soppet, D.R.,
Moore, P.A., Shi, Y., Lafleur, D.W., Olsen, H.S., Florence, K.A. and
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HUMAN GENOME SCIENCES INC
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PR 10-FEB-1999 US 60/119468
PI CRAIG A ROSEN, STEVEN W RUBEN, REINHARD EBNER, PAUL E YOUNG, JIAN
NI,
PI DANIEL R SOPPET, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR, HENRIK
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 REFERENCE
 AUTHORS Young, P., Greene, J.M., Fertle, A.M., Ruben, S.M., Rosen, C.A.,
 Duan, R.D., Hu, J.S., Florence, K.A., Olsen, H.S., Ebner, R.,
 Brewer, L.A., Moore, P.A., Shi, Y., Lafleur, D.W. and N.J.
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 YOUNG, JOHN M GREENE, ANN M FERRIE, STEVEN M RUBEN, CRAIG A PI
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 REFERENCE 1 (bases 1 to 1352)
 Bouchon, A., Cell, M., Grierson, H.L., Cohen, J.I. and Colonna, M.
 Cutting Edge: Activation of NK Cell-Mediated Cytotoxicity by a
 SAP-Independent Receptor of the CD2 Family
 J. Immunol. 167 (2001) In press
 2 (bases 1 to 1352)
 Colonna, M.
 Direct Submision
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 Best Local Similarity 99.6%; Pred. No. 0;
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 QY 22 GCTGACTTCAG 81
 Db 1 GCTGACTTCAG 60
 QY 82 TTTGACAGTCAAG 141
 Db 61 TTTGACAGTCAAG 120
 QY 142 GTGGGCGGTGACTTCCCGTGAAGTCCAAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 201
 Db 121 GTGGGCGGTGACTTCCCGTGAAGTCCAAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 QY 202 CTTTCAACAGAACCCCTCTGTCAATATACAGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 261


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Db      181 CTTTCAACACACACCCCTCTGTCAACCATACAGCCAGAGGGGGGACATCATATGTGACC 240
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Db      241 AAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTACTCCCTGAAGTCAACA 300
Qy      322 AACGAAAGAAATGATCTCAGGAGTCACTATGAGGGGATATACAGTCAATCACTCAGC 381
Db      301 AACGAAAGAAATGATCTCAGGAGTCACTATGAGGGGATATACAGTCAATCACTCAGC 360
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Qy      442 CCAATGGGTCTGACAGCAATAGAAATGACACTGTGTGACCAATCTGACATGCTGAC 501
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Qy      562 CCCATATGGGTCCATCTCCCATCTCTGAGAGTGGGAGAAAGTATGATGACCTTCA 621
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Qy      622 TCTGCGTGGCAGAGAACCTGTGACAGAGAACTTCTCAAGCCCATCTTGGCCAGAGAC 681
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Qy      682 TCTGTGAAGGTGCTGCTGATGACCCAGATTCCTCCATGCTCTCTGTGCTCTGTTGG 741
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Qy      742 TGCCCTCTCTGCTCAGTCTCTTGTATCTGGGGCTATTTCTTGGTTCTGAAGAGAGA 801
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Qy      802 GACAAAGAGATCATTGAAGAGAGAGAGATGACATTTGTGGGAAACTCTCTAACA 861
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Qy      862 TATGCCCTCTCTGCTGAGAGACACAGAGTACCAATCTCTCACTAATATGAACA 921
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Qy      922 TCCTAAAGAGAGATCCAGCAAACTACGTTTACTCCTGAGAAATACCGAAAAAGATGG 981
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Qy      982 AAAATCCCACTACCTGCTCAGATGTCAGACACCAAGGCTATTTGCTATGAGATG 1041
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Db      1201 ATTTCATCCACTGCTGAGAAATCTCTCAAAACCAAGAGTTTAAATCACTTATCCCAA 1260
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Db      1261 AATGGATTTGTAATGTCAGCAAAACCATTAATAAAAGTGCTTAGAAGTATCTTATTAATA 1320
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Db      1321 TGTAAATGCAATGT 1334

RESULT 13
HSM804336
LOCUS      HSM804336      1250 bp      mRNA      linear      PRI 10-JUL-2002
DEFINITION Homo sapiens mRNA; cDNA DKFP666F188 (from clone DKFP666F188).
ACCESSION AL833025
VERSION    AL833025.1 GI:21733615
KEYWORDS
SOURCE
ORGANISM  Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS   Anstorge, W., Markner, U., Mewes, H.W., Weil, B. and Wiemann, S.
TITLE     Direct Submission
JOURNAL   Submitted (09-JUL-2002) 1, D-85764 Neuberberg, GERMANY
COMMENT   Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFP666F188) is available at the RZPD in Berlin.
            Please contact the RZPD: Reissourcentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.

FEATURES
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/organism="Homo sapiens"
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DH10B; sites NotI + SalI"
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polya_signal
1210..1215
polya_site
1239

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Matches 1239; Conservative 0; Mismatches 6; Indels 8; Gaps 4;

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Qy      1510 GCAGATGACCTGACCAAAAAATGATATTAATGCTCTTATTAATTAATGCTGCCAGCAC 1569
Db      61 GCAGATGACCTGACCAAAAAATGATATTAATGCTCTTATTAATTAATGCTGCCAGCAC 120
Qy      1570 TATGCTGAGGCTTACCTAATTTGGTCAAGAGTGTCTGCTGCCCTCATGAATTTGGCTCAA 1629
Db      121 TATGCTGAGGCTTACCTAATTTGGTCAAGAGTGTGTCTGCTGCCCTCATGAATTTGGCTCAA 180
Qy      1630 ATGAATGAACCTACTTTTCAATGAGCAGTTGTAGCAGGCTGACCAAGATTCACAGAGGCC 1689
Db      181 ATGAATGAACCTACTTTTCAATGAGCAGTTGTAGCAGGCTGACCAAGATTCACAGAGGCC 240
Qy      1690 AGGTGATGATCCACAGAGCTTGAAGTCAAAAGTTCAAAAGATGAAGATTCAGGATGCT 1749
Db      241 AGGTGATGATCCACAGAGCTTGAAGTCAAAAGTTCAAAAGATGAAGATTCAGGATGCT 300
Qy      1750 GACCATGTTTGGCAGATTAATTAATGAGACACAGAAAGTGTGATGCGCCCAAGACAGAG 1809

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Db 301 GACCATGTTGGCAGATTAATTAATGAGACACAGAAAGTGTGATGAGCCCAAGACAG 360
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Db 361 ACCTCAGCAGGAGCTTCAATTAATGACCTGTGTGCAAAAAGAAAGTATAGTTTAAAG 420
Qy 1870 CTGTGCGAAGAACCCATCCCAATTAAGAGACCGAGTCTGAAGTCAATGTAAATCTAGTG 1929
Db 421 CTGTGCGAAGAACCCATCCCAATTAAGAGACCGAGTCTGAAGTCAATGTAAATCTAGTG 480
Qy 1930 TAGGACATTTGAGTGAAGGAGTGAAGTGTGTGGGCAAGGGGGGAGTGGGATCTTGA 1989
Db 481 TAGGACATTTGAGTGAAGGAGTGAAGTGTGTGGGCAAGGGGGGAGTGGGATCTTGA 540
Qy 1990 AACCTTTAAGATGTTAATTAATCAATAGATATTAATTAAGAACTTATGCGGCC 2049
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Qy 2050 GGCATGTGGCTCAACCTGTAAATCCAGACCTTTGGAGGCCAAGTGGGTGGTCAATC 2109
Db 598 GGCATGTGGCTCAACCTGTAAATCCAGACCTTTGGAGGCCAAGTGGGTGGTCAATC 657
Qy 2110 TAGAGTCAGAGATTCAGAACCAAGCTGGCCCAATGTGTAACCCATCTCTAATAAGA 2169
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Qy 2170 T--CAAAATTTGTGACGCTGTGTGTGCACTGT-ATCCAGCTACTCGAAGGCCAA 2226
Db 718 TACAAAATTTGTGACGCTGTGTGTGCACTGTATCCAGCTACTCGAAGGCCAA 777
Qy 2227 GGCATGAGAAATCGCTTGAACCTGG--AGGTAGGTTCAGTGTGAGTGTGACCACT 2284
Db 778 GGCATGAGAAATCGCTTGAACCTGGAGGTGTGAGTGTGAGTGTGACCACT 837
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Qy 2525 AACCAATGCTGTGTGGCAAGAAATGGGATTTATCTTCTCAGAAAAGCATTTGT 2584
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Qy 2585 GAAAGATTTGAGCAGATCTCTCTCTAATGCAAAACCTTAATTTGATTAAGTCTT 2644
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RESULT 14

AR252549 1076 bp DNA 1linear PAT 20-DEC-2002
LOCUS AR252549
DEFINITION Sequence 252 from patent US 6478825.
ACCESSION AR252549
VERSION AR252549.1 GI:27300457
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 1076)
AUTHORS Winerebottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the
JOURNAL treatment of bone defects
FEATURES Patent: US 6478825-A 252 12-NOV-2002;
source Location/Qualifiers
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Query Match 39.8%; Score 1076; DB 6; Length 1076;
Best Local Similarity 100.0%; Pred. No. 2,3e-293;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 65 CACCTCATCTATATCTTTTGGCAGCTGACAGGCTCAGAGCTTGGACCCGTGAAGA 124
Db 61 CACCTCATCTATATCTTTTGGCAGCTGACAGGCTCAGAGCTTGGACCCGTGAAGA 120
Qy 125 GCTGGTCCGTTCCGTTGGTGGGCGGTGACTTTCCCTGAAGTCCAAAGTAAACAACT 184
Db 121 GCTGGTCCGTTCCGTTGGTGGGCGGTGACTTTCCCTGAAGTCCAAAGTAAACAACT 180
Qy 185 TGACCTATATGCTGAGACCTTCAACAAACCCCTGTGTACATACAGCCAGAGGGGG 244
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Qy 245 CACTATCATATGAGCCCAAAATCTATATAGGAGAGATGAGCTTCCAGATGAGGCTA 304
Db 241 CACTATCATATGAGCCCAAAATCTATATAGGAGAGATGAGCTTCCAGATGAGGCTA 300
Qy 305 CTCCCTGAAGCTCAGCAAACTGAAAGAAATGACTCAGGATCTATATGTGGGATATA 364
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Qy 365 CAGCTCATCATCCAGAGAGCCCTCCAGCCAGAGATGAGTGTGATCAGACACT 424
Db 361 CAGCTCATCATCCAGAGAGCCCTCCAGCCAGAGATGAGTGTGATCAGACACT 420
Qy 425 GTCAAAAGCTTAAGTACCATGGGTCTGACAGCAATTAAGATGGACCTGTGTACCA 484
Db 421 GTCAAAAGCTTAAGTACCATGGGTCTGACAGCAATTAAGATGGACCTGTGTACCA 480
Qy 485 TCTGACATGCTGATGAAATCATGGGAAAGAGATGTATTTATCTGGAAGGCTTGG 544
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Qy 545 GCAAGCAGCAATGAGTCCCAATATGGGTCCATCTCCCAATCTCTGGAATGGGGAGA 604
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Qy 665 CATCTTCGACAGAAAGCTCTGTGAAGGTGCTGTGATGACCAATTTCTTCATGTCT 724
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Db 721 CCTGTGTCCTGTTGGTGGCCCTCTCTGCTAGTCTCTTTGATCTGGGGCTATTTCTTTG 780
Qy 785 GTTCTGGAAGAGAGACAAAGAGATTAATTAAGAAAGAAAGAGAGTGAATTTG 844
Db 781 GTTCTGGAAGAGAGACAAAGAGATTAATTAAGAAAGAAAGAGTGAATTTG 840
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RESULT 15
AX092314 1076 bp DNA linear PAT 21-MAR-2001
LOCUS AX092314
DEFINITION Sequence 45 from Patent WO0116318.
ACCESSION AX092314
VERSION AX092314.1 GI:13444471
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Chordata; Craniata; Vertebrata; Euteleostomi;
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
            Euton,D.L., Pilvaroff,E., Gerritsen,M.B., Goddard,A.,
            Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
            Wood,M.I.
            Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL Patent: WO 0116318-A 45 08-MAR-2001;
            Genentech, Inc. (US)
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ORIGIN
Query Match          39.8%; Score 1076; DB 6; Length 1076;
Best Local Similarity 100.0%; Pred. No. 2,3e-293;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 GTGGCTTCATTTCAGTGGCTGACTTCCAGAGACAAATATGCTGTTCCCAACATGCT 64
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Qy      65 CACCCATCATCTATATCCTTTGGGAGCTCAGAGGTGACAGCCCTTGAGACCCGGTGAAGA 124
Db      61 CACCCATCATCTATATCCTTTGGGAGCTCAGAGGTGACAGCCCTTGAGACCCGGTGAAGA 120
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Db      121 GCTGTCGCTTCGTTGGTGGGCGCTGACTTTCCCTGAAGTCAAAAGTAAAGCAAGT 180
Qy      185 TGACTCTATTGTCGACCTTCAACACACACCCCTTTGTCAACATACAGCCAGAGGGGG 244
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Db      481 TCTGACATGCTGATGAAACATGAGGAGAGATGATTTATTAATCTGAGAGCCCTGGG 540
Qy      545 GCAGAGCCCAATGATGCCCATTAATGGGTCCATTCCTCCCATCTCTCGAGATGGGAGA 604
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Qy      725 CTTGTGCTCTCTGTGGTGGTCCCTCTGCTCAAGTCTTTGTACTGGGGTATTTCTTGG 784
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Db      961 AATACCGAAAAAGATGAAAAATCCCACTCACTGCTGACATGCGACAGACACCAAGGCT 1020
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 03:55:11 ; Search time 8248 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	776.4	28.7	784	CD364928	CD364928 UT-H-PT2-
3	761.2	28.2	785	CD366908	CD366908 UT-H-PT2-
4	760	28.1	1035	BM549599	BM549599 AGENCOURT
5	746.6	27.6	876	BU166292	BU166292 AGENCOURT
6	734.2	27.2	846	BG743877	BG743877 602722632
7	734.2	27.2	1043	BQ053807	BQ053807 AGENCOURT
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9	732.8	27.1	904	BQ712547	BQ712547 AGENCOURT
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12	728.8	27.0	749	CD366342	CD366342 UT-H-PT2-
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30	605	22.4	968	5	BQ898498
31	604.2	22.3	670	4	BG744563
32	600.8	22.2	648	6	CD687842
33	596.2	22.0	602	1	AI638519
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35	589	21.8	553	2	BE326659
36	584	21.6	760	6	CB956896
37	582.4	21.5	774	5	BU183701
38	573.6	21.2	935	2	BF027036
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41	522.2	19.3	527	1	AI968397
42	516.4	19.1	534	2	AM293413
43	508	18.8	614	1	AV733301
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45	494	18.3	855	5	BQ440846

ALIGNMENTS

RESULT 1
BM551726
LOCUS BM551726 1026 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6544759 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548139
5', mRNA sequence.
BM551726
VERSION BM551726.1 GI:18788997
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM12256 row: j column: 12
High quality sequence stop: 552.
Location/Qualifiers
1..1026
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/db_xref="taxon:9606"
/clone="IMAGE:5548139"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT; Site: 1: NciI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

FEATURES

source

ORIGIN

Query Match 30.3%; Score 818.4; DB 4; Length 1026;
Best Local Similarity 96.4%; Pred. No. 4.6e-137;
Matches 890; Conservative 0; Mismatches 24; Indels 9; Gaps 5;

1786 AGTGTGATGGCCCAAGACAGACCTCAGCAGCTTCAATTATGCACTGTGCTGC 1845

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Db      1 AGGTGCATGGCCCAAGACAAAGACCTCCAGCCAGGCTTCATTATGCACTGTGCTGC 60
QY      1846 AAAAGAAAAGCTCAAGTTTTTAAGAGCTGTGCCAAGAACCCATCCCAATAAAGAGCCCAAGTC 1905
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Db      121 TGAAGTCACATTTGTAATATCTAGTGTAGAGACTTGTGAGTCAGGACAGTGTGAGTGTGAGG 180
QY      1966 CACGGGGGGAGTGGGTACTTGTAAACCTTTAAAGATGGTTAATTCATTCAATAGATAT 2025
Db      181 CACGGGGGGAGTGGGTACTTGTAAACCTTTAAAGATGGTTAATTCATTCAATAGATAT 240
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Db      241 TATTAGAAGCTATCTATGAGCGCCCGGCAATGTGGCTCACACCTGTAAATCCCAAGACTTTG 297
QY      2086 GGAGGCCAAGTGGGTGGTCACTGTAGGTCAAGAGTTCAAGACCAAGCTGGCCCAATG 2145
Db      298 GGAGGCCAAGTGGGTGGTGGTCACTGTAGGTCAAGAGTTCAAGACCAAGCTGGCCCAATG 357
QY      2146 GTGAAACCCCATCTCTACTAATAAGAT--CAAAATTTGCTGAGCGTGGTGTGACCTGT 2203
Db      358 GTGAAACCCCATCTCTACTAATAAGATCAAAAATTTGCTGAGCGTGGTGTGACCTGT 417
QY      2204 -ATCCAGTACTCTGAGAGGCCCAAGGACATGAGATAGGCTTGAACCTGG--AGTGAAGTT 2260
Db      418 AATCCAGTACTCTGAGAGGCCCAAGGACATGAGATAGGCTTGAACCTGGAGGTGAGGTT 477
QY      2261 GCAGTGAAGTGAAGTGGCACTGTCACCTCGGCTGAGGCAACGAGAGCAAAATCTCAAT 2320
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QY      2321 ACAACAAACAAACAAACACCTGTGCTGAGTCACTGTGCACTGAATGAATGATCCCTTA 2380
Db      538 ACAACAAACAAACAAACACCTGTGCTGAGTCACTGTGCACTGAATGAATGATCCCTTA 597
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Db      598 CCAACACAGAGCTCACATCTCTTAATCACTTAAGTGAAGAAACATGGGGAAGGGGAAGGGG 657
QY      2441 AATGCTGCTTTGATATGTCTCCCTGACGCAATCTTGAATGAGAGACTCCCTACCAAGT 2500
Db      658 AATGCTGCTTTGATATGTCTCCCTGACGCAATCTTGAATGAGAGACTCCCTACCAAGT 717
QY      2501 GATGAAAGTGTGAAACCTTAATAACAATGCTTGTGGGCAAGATGGGATTTGAGAT 2560
Db      718 GATGAAAGTGTGAAACCTTAATAACAATGCTTGTGGGCAAGATGGGATTTGAGAT 777
QY      2561 TATCTCTCTCAAGAAAGGATTTGTAAGAAATGAGCCAGATCTCTCCCTACCTGCAAA 2620
Db      778 TATCTCTCTCAAGAAAGGATTTGTAAGAAATGAGATCTCTCCCTACCTGCAAA 837
QY      2621 ACCCTATTTAGTAAAGAGTCTTCTTACTATCTTAATTAACAGATATTTGAGATTC 2680
Db      838 ACCCTATTTAGTAAAGAGTCTTCTTACTATCTTAATTAACAGATATTTGAGATTC 896
QY      2681 ACATATAAAAAAAAAAAAAAAAAA 2703
Db      897 NCCGTACCAAGAAAAA 919

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RESULT 2
CD364928/c 784 bp mRNA linear EST 05-AUG-2004
LOCUS      UI-H-FT2-bjn-g-19-0-UI-s1 NCI CGAP FT2 Homo sapiens cDNA clone
DEFINITION UI-H-FT2-bjn-g-19-0-UI 3', mRNA sequence.
ACCESSION  CD364928
VERSION     CD364928.1 GI:31149018
KEYWORDS    EST.
SOURCE      Homo sapiens (human)

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ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 784)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           Tissue Procurement: Dr. Gary W. Hunninghake, U of I
           cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
           DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
           Clone Distribution: Distribution information can be found at
           http://genome.uiowa.edu/distribution/cgap.html
           Seq primer: M13 FORWARD
           POLYA=yes.

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FEATURES
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    /mol_type="mRNA"
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    /lab_host="DH10B (Life Technologies)"
    /clone_id="NCI-CGAP-FT2"
    /note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a
    modified polylinker; Site_1: EcoR I; Site_2: Not I;
    NCI-CGAP FT2 is a subcloned cDNA library constructed from
    a pool of 81 RNA samples from Alveolar Macrophages
    challenged with different treatments. The mRNA samples
    were a mixture of these conditions (times refer to
    incubations following isolation by bronchoalveolar lavage)
    (some normal donor macrophages were cultured in some of
    the conditions, other donor macrophages in different
    conditions). The mRNA samples were pooled for library
    construction. Control 0 hours; control 3 hours; control 24
    hours; LPS 100 ng/ml; 3 hours; LPS 100 ng/ml; 24 hours;
    PMA 10 ng/ml; 3 hours; PMA 10 ng/ml; 24 hours; Klebsiella
    moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph
    aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
    Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
    Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
    adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
    hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
    wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
    The library was subcloned according to Bonaldo, Lennon
    and Soares, Genome Research, 6:791-806, 1996. The tissue
    was provided by Dr. Gary W. Hunninghake of the University
    of Iowa.
    TAG_TISSUE=Human Lung Alveolar Macrophage
    TAG_LIB=UI-H-FT2
    TAG_SEQ=GGCCATGCCG"

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ORIGIN

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Query Match      28 7%; Score 776.4; DB 6; Length 784;
Best Local Similarity 99.7%; Pred. No. 1.7e-125;
Matches 777; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      764 GCTGCAGAACTGAGAGAAATGACTCAGGATCTACTATGTGGGATATACAGCTCATC 725
QY      374 ACTCCAGAGCCCTCCACCCAGAGATGCTGCTGATCTTACAGCACTGTCAAAAGCC 433
Db      724 ACTCCAGAGCCCTCCACCCAGAGATGCTGCTGATCTTACAGCACTGTCAAAAGCC 665
QY      434 TTAAGTCAACATGGGTCTGCAAGCAATTAAGAAATGGCACTGTGACCAATCTGATC 493
Db      664 TTAAGTCAACATGGGTCTGCAAGCAATTAAGAAATGGCACTGTGACCAATCTGATC 605

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QY 494 CTGCATGAAATGAGGAGAGATGATTTATACCTGAAAGCCCTGGGGCAAGAGC 553
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 QY 554 CAATGAGTCCCATTAATGGGTCATCTCCCATCTCTGGAGATGGGAGAAATGATAT 613
 DB 544 CAATGAGTCCCATTAATGGGTCATCTCCCATCTCTGGAGATGGGAGAAATGATAT 485
 QY 614 GACCTTATCTGGGCTTCCAGGAAACCTGTGAGAGAAATCTTCAAGCCCATCTGC 673
 DB 484 GACCTTATCTGGGCTTCCAGGAAACCTGTGAGAGAAATCTTCAAGCCCATCTGC 425
 QY 674 CAGGAACCTCTGTGAGAGTGTCTGATGAGCCAGATTCCTCATGTCTCTGTCT 733
 DB 424 CAGGAACCTCTGTGAGAGTGTCTGATGAGCCAGATTCCTCATGTCTCTGTCT 365
 QY 734 CTTGTGTGTCCT 793
 DB 364 CTTGTGTGTCCT 305
 QY 794 GAG 853
 DB 304 GAG 245
 QY 854 TCCTTAATATAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 913
 DB 244 TCCTTAATATAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 185
 QY 914 TAGAACAATCTTAAGAGAGATTCAGCAAAATACGTTTACTCACTGTGAAATACGAA 973
 DB 184 TAGAACAATCTTAAGAGAGATTCAGCAAAATACGTTTACTCACTGTGAAATACGAA 125
 QY 974 AAAGATGAAATATCCCACTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1033
 DB 124 AAAGATGAAATATCCCACTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 65
 QY 1034 TGAGATGTTATCTAGACAGAGTGCATCCCTTAAGTCTCTCTCTCTCTCTCTCT 1092
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RESULT 3
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 LOCUS UT-H-FT2-bjp-a-22-0-UI.81 NC1_GCAP_F12 Homo sapiens cDNA clone
 DEFINITION UT-H-FT2-bjp-a-22-0-UI 3', mRNA sequence.
 ACCESSION CD366908
 VERSION CD366908.1 GI:31150998
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 785)
 NC1_GCAP <http://www.ncbi.nlm.nih.gov/nc1gap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES
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/clone="UI-H-FT2-bjp-a-22-0-UI"
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 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
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 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
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 NC1_GCAP_F12 is a subcloned cDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages
 challenged with different treatments. The mRNA samples
 were a mixture of these conditions (times refer to
 incubations following isolation by bronchoalveolar lavage)
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
 moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph
 aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
 Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
 Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
 adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
 wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
 The library was subcloned according to Bonaldo, Lennon
 and Soares, Genome Research, 6:791-806, 1996. The tissue
 was provided by Dr. Gary W. Hunninghake of the University
 of Iowa.
 TAG_TISSUE=Human Lung Alveolar Macrophage
 TAG_L1B=UI-H-FT2
 TAG_SEQ=GGCCATGCCG"

ORIGIN
 Query Match 28.2%; Score 761.2; DB 6; Length 785;
 Best Local Similarity 99.1%; Pred. No. 9.3e-127;
 Matches 774; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 312 AACCTAGCAAACTGAAAGAGATGACTACGAGATCTATCTGGGATATACAGTCA 371
 DB 785 AACCTAGCAAACTGAAAGAGATGACTACGAGATCTATCTGGGATATACAGTCA 727
 QY 372 TCACTCCAGAGCCCTCCACCCAGAGATGCTGATGTCTACGAGACCTGTCAAG 431
 DB 726 TCACTCCAGAGCCCTCCACCCAGAGATGCTGATGTCTACGAGACCTGTCAAG 667
 QY 432 CCTAAGTCAATGGGTCTGACAGCAATAGATGCACTGTGTGACCAATCTTGACA 491
 DB 666 CCTAAGTCAATGGGTCTGACAGCAATAGATGCACTGTGTGACCAATCTTGACA 607
 QY 492 TGTGATGGAATAGGGAGAGAGATGATTTAATCTTGGAAGGCCCTGGGCAAGCA 551
 DB 606 TGTGATGGAATAGGGAGAGAGATGATTTAATCTTGGAAGGCCCTGGGCAAGCA 547
 QY 552 GCCAATGAGTCCATATAGGGTCCATCTCCCATCTCCCTGGAGATGGGAGAAAGTAT 611
 DB 546 GCCAATGAGTCCATATAGGGTCCATCTCCCATCTCCCTGGAGATGGGAGAAAGTAT 487
 QY 612 ATGACCTTATCTGCGTTGACAGAAACCTGTGAGAGAAATCTTCAAGCCCATCTCT 671
 DB 486 ATGACCTTATCTGCGTTGACAGAAACCTGTGAGAGAAATCTTCAAGCCCATCTCT 427
 QY 672 GCCAGAGAGTCTGTGAGAGTGTCTGATGAGCCAGATTCCTCATGTCTCTGTGT 731
 DB 426 GCCAGAGAGTCTGTGAGAGTGTCTGATGAGCCAGATTCCTCATGTCTCTGTGT 367
 QY 732 CTCCTGTGTGTCCT 791
 DB 366 CTCCTGTGTGTCCT 307
 QY 792 AAGAGAGAGAGAGAGAGAGATCATTTAAGAGAGAGAGAGAGATTTGTGGGAA 851
 DB 306 AAGAGAGAGAGAGAGAGAGATCATTTAAGAGAGAGAGAGAGATTTGTGGGAA 247

QY 852 ACTCTACATATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACAAATCCCTCACACT 911
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Db 246 ACTCTACATATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACAAATCCCTCACACT 187
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QY 912 AATAGAACATCTCTAAAGAGAGATCCAGCAATACGTTTACTCTCACTGTGGAATACCG 971
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Db 186 AATAGAACATCTCTAAAGAGAGATCCAGCAATACGTTTACTCTCACTGTGGAATACCG 127
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QY 972 AAAAAATGGAATAATCCCATCTGCTCAGATGCGAGACACCAAGGCTATTGGC 1031
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Db 126 AAAAAATGGAATAATCCCATCTGCTCAGATGCGAGACACCAAGGCTATTGGC 67
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QY 1032 TATGAGATGTTATCTAGACAGAGTGCCTCCCTTAAGTCTGCTCAAAAAAACA 1091
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QY 1092 A 1092
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Db 6 A 6
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LOCUS BMS49959
DEFINITION AGENCOURT_6544167 NIH_MGC_118 Homo sapiens CDNA clone IMAGE:5745910
5', mRNA sequence.
ACCESSION BMS49959
VERSION BMS49959.1 GI:18785781
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1035)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL12769 row: j column: 23
High quality sequence start: 12
High quality sequence stop: 663.
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/note="Vector: pCMV-SPORT6, Site 1: NotI, Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

ORIGIN
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Best Local Similarity 99.2%; Pred. No. 1.4e-126;
Matches 774; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Db 23 AATATGCTGTTTCCCAACATGCTCAACCTCATATATCTTTGGAGCTCAGAG 82
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QY 99 TCAGAGCTCTGAGACCGGTGAAGAGCTGGTCCGTTGGTGGGCGCTGACTTC 158
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Db 83 TCAGAGCTCTGAGACCGGTGAAGAGCTGGTCCGTTGGTGGGCGCTGACTTC 142
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QY 159 CCCCGAAGTCCAAAGTAAAGATGACTATATGCTGGACCTTCAACCAACCT 218
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Db 143 CCCCGAAGTCCAAAGTAAAGATGACTATATGCTGGACCTTCAACCAACCT 202
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QY 219 CTGTGACCATGACAGCCAGAGGGGCACTATCATATGAGCCCAAAATGTAATAGGAG 278
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Db 203 CTGTGACCATGACAGCCAGAGGGGCACTATCATATGAGCCCAAAATGTAATAGGAG 262
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QY 279 AGAGTAGACTTCCAGATGAGGCTTACTCCCTGAAAGCTCAGCAAACTGAAGAATGAC 338
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Db 263 AGAGTAGACTTCCAGATGAGGCTTACTCCCTGAAAGCTCAGCAAACTGAAGAATGAC 322
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QY 339 TCAGGATCTATATGTTGGGATATACAGCTCATCTCCAGACCTCCACCCAGAG 398
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Db 323 TCAGGATCTATATGTTGGGATATACAGCTCATCTCCAGACCTCCACCCAGAG 382
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QY 399 TACGTGCTGATGCTTACAGAGCCTGTCAAAAGCTTAAGTCAACCATGGGTCTGAGAGC 458
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|
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Db 383 TACGTGCTGATGCTTACAGAGCCTGTCAAAAGCTTAAGTCAACCATGGGTCTGAGAGC 442
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QY 459 AATAGAAATGGCACTGTGTGTCACAACTGATGCTGATGGAACATGGGGAGAAGAT 518
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QY 699 GATGACCAAGATTCCTCATGCTCTCTGTGTCCTGTTGGTGGCCCTCTGCTCAGT 758
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Db 683 GATGACCAAGATTCCTCATGCTCTCTGTGTCCTGTTGGTGGCCCTCTGCTCAGT 741
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Db 742 CTCTTTGACTGGGCTATTTCTTTGTTTCTGAAGAGAGAGACAGAAAGATACATT 801
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RESULT 5
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LOCUS BU166292
DEFINITION AGENCOURT_7944604 NIH_MGC_72 Homo sapiens CDNA clone IMAGE:6148660
5', mRNA sequence.
ACCESSION BU166292
VERSION BU166292.1 GI:22680244
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 876)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM13480 row: h column: 05
 High quality sequence stop: 724.
 Location/Qualifiers

FEATURES

source

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 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: Skin; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

ORIGIN

Query Match 27.6%; Score 746.6; DB 5; Length 876;
 Best Local Similarity 97.3%; Pred. No. 3.8e-124;
 Matches 823; Conservative 0; Mismatches 15; Indels 8; Gaps 6;

Qy 947 GGTTCCTCCAGTGTGAAATACCGAAAGATGAAATCCCACTCAGTCTGACAGAT 1006
 Db 1 GGTTCCTCCAGTGTGAAATACCGAAAGATGAAATCCCACTCAGTCTGACAGAT 60
 Qy 1007 GCCAGACACCAAGGCTATTTGGCTATGAAATGTTATCTAGACAGACAGTCCCTCC 1066
 Db 61 GCCAGACACCAAGGCTATTTGGCTATGAAATGTTATCTAGACAGACAGTCCCTCC 120
 Qy 1067 TAACTCTGCTCAAAAAAACAATCTTCGCCCAAGAAAACAATCAGAAAGATTC 1126
 Db 121 TAACTCTGCTC-AAAAAACAATCTTCGCCCAAGAAAACAATCAGAAAGATTC 179
 Qy 1127 CTGATTGACTAGAAACATCAAGAAAGAAAGAAAGCTGACCTTTTCCAGATTAAT 1186
 Db 180 CTGATTGACTAGAAACATCAAGAAAGAAAGAAAGCTGACCTTTTCCAGATTAAT 239
 Qy 1187 TATCTCGATGCTCTTAAAGTTAAGATTCGTAATCCATCCAGTCTGAGAAATCTC 1246
 Db 240 TATCTCGATGCTCTTAAAGTTAAGATTCGTAATCCATCCAGTCTGAGAAATCTC 299
 Qy 1247 CTCAAACCCAGAAAGTTAATCACTTCATCCAAAAATGGATTTGATGTCAGCAAC 1306
 Db 300 CTCAAACCCAGAAAGTTAATCACTTCATCCAAAAATGGATTTGATGTCAGCAAC 359
 Qy 1307 CATTAATAAAAGTGTGAAGTATTCCTATTAAGAAATGAATGCAAGTCAACATTTA 1366
 Db 360 CATTAATAAAAGTGTGAAGTATTCCTATTAATAAATGAATGCAACATTTA 419
 Qy 1367 ATGACAGCTGTTGATTAATGATGCTCCAGGTCAGTGTGAGTTTCATTCATCC 1426
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Db 660 TGCCCTGATGAATTTGGCTCCAAATGAATGAACTACTTTCATGAGCAGTTAGCAGGCC 719
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 Db 840 GACACA 845

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 BG743877.1 GI:14054530
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 BG743877.1
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 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 846)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT
 Contact: Robert Straube, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM1688 row: 0 column: 07
 High quality sequence stop: 782.
 Location/Qualifiers

FEATURES

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 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH-MGC library."

ORIGIN

Query Match 27.2%; Score 734.2; DB 4; Length 846;
 Best Local Similarity 93.5%; Pred. No. 6.5e-122;
 Matches 788; Conservative 0; Mismatches 53; Indels 2; Gaps 2;

Qy 908 CACTAATAGAACATCTTAAGAGATCCAGCAATAGCGTTACTCCATGTGAAAT 967
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 Qy 968 ACCGAAAAAGATGGAATATCCCACTCAGTCTCAGATGCCAGACACCAAGGCTATT 1027
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RESULT 7
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 DEFINITION 5', mRNA sequence.
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 VERSION B0053807.1 GI:19813147
 KEYWORDS EST.
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1043)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
 cDNA Library Preparation: Rubin Laboratory

cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM2123 row: n column: 22
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 /note="Organ: blood; Vector: pORB7, Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN
 Query Match 27.2%; Score 734.2; DB 5; Length 1043;
 Best Local Similarity 98.2%; Pred. No. 6.3e-122;
 Matches 753; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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 QY 428 AAGCCTTAAGTCCACATGAGTCTGCAAGCAATAAGATGACCTGTCATCAATCT 487
 DB 61 AAGCCTTAAGTCCACATGAGTCTGCAAGCAATAAGATGACCTGTCATCAATCT 120
 QY 488 GACATGCTGATGAAATGAGGAGAGAGATGTAATTAATACCTGGAAGGCTGAGGCA 547
 DB 121 GACATGCTGATGAAATGAGGAGAGAGATGTAATTAATACCTGGAAGGCTGAGGCA 180
 QY 548 AGCAGCCAAATGAGTCCCAATATGAGTCAATCTCCCATCTCTGAGATGAGGAGAAAG 607
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QY 1028 TGCCATGAGAAATGTATCTAGACAGAGTCACTCCCTCAAGTCTGCTCAAAAAA 1087
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 ACCESSION CBS29471 GI:29390191
 VERSION CBS29471.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 767)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapdb-remail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.iowa.edu/distribution/cgap.html
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 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
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 NCI CGAP FT2 is a subcloned cDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages
 challenged with different treatments. The RNA samples
 were a mixture of these conditions (times refer to
 incubations following isolation by bronchoalveolar lavage)
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
 moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph
 aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
 Adenoviral vector (Ad5 CMV egfp), moi 500, 3 hours;
 Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; wt
 adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
 wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
 The library was subcloned according to Bonaldo, Lennon
 and Soares, Genome Research, 6:791-806, 1996. The tissue
 was provided by Dr. Gary W. Hunninghake of the University
 of Iowa.
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 TAG_LIB=ui-H-FT2

ORIGIN TAG_SEQ=GGCCATGCCG"
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 VERSION B0712547.1 GI:21851446
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 904)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabers-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LNCM2521 row: m column: 15
High quality sequence stop: 637.
Location/Qualifiers

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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."

ORIGIN

Query Match

Best Local Similarity 91.6%; Score 732.8; DB 5; Length 904;
Pred. No. 1.2e-121;
Matches 826; Conservative 0; Mismatches 32; Indels 44; Gaps 3;

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KEYWORDS EST.
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 793)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gtu@incyte.com.

FEATURES
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Query Match 27.1%; Score 731.8; DB 6; Length 793;
Best Local Similarity 98.7%; Pred. No. 1.8e-121;
Matches 769; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

741 GTGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800
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DB 668 CAGTGTCTGAGATTTCATTCATCCAGAGGCTGTGATGTCAAGATTAATCAAGAGTCTT 727
QY 1461 GCTACCAAGAGGCGCAAAAGCAAAACAGACAGACAGTCCAGCAAGATGAC 1519
DB 728 GCTACCAAGAGGCGCAAAAGCAAAACAGACAGACAGTCCAGCAAGATGAC 786

RESULT 11
CD364943/c 738 bp mRNA linear EST 05-AUG-2004
LOCUS CD364943
DEFINITION UI-H-FT2-bj-h-k-01-0-UI.s1 NCI_CGAP_F12 Homo sapiens cDNA clone
VERSION UI-H-FT2-bj-h-k-01-0-UI 3', mRNA sequence.
KEYWORDS CD364943.1 GI:31149033
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 738)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strauberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
PolyA-yes.
FEATURES
Source Location/Qualifiers
1..738
/organism="Homo sapiens"
/mol_type="mRNA"

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/db_xref="taxon:9606"
/clone="UI-H-FT2-bj-h-k-01-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1ib="NCI_CGAP_F12"
/notes="Organ: Lung; Vector: pTR73-Pac (Pharmacia) with a
modified polylinker, Site 1: EcoR I, Site 2: Not I;
NCI_CGAP_F12 is a subtracted cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The RNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph
aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
Adenoviral vector (Ad5 CMV egfp), moi 500, 3 hours;
Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; wt
adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
The library was subtracted according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. The tissue
was provided by Dr. Gary W. Hunninghake of the University
of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_L1ib=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match 27.0%; Score 728.8; DB 6; Length 738;
Best Local Similarity 99.6%; Pred. No. 6,3e-121;
Matches 730; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 360 ATATACAGCTCATCTCCAGACAGCCCTCCAGAGAGTACGCTGATGCTACGAG 419
DB 738 ATATACAGCTCATCTCCAGACAGCCCTCCAGAGAGTACGCTGATGCTACGAG 679
QY 420 CACCTGTCAAAGGCTTAAGTCAACCATGAGGCTGCTCAAGCAATTAAGTGGACCTGTG 479
DB 678 CACCTGTCAAAGGCTTAAGTCAACCATGAGGCTGCTCAAGCAATTAAGTGGACCTGTG 619
QY 480 ACCAATCTGACATGCTGATGGAACATGGGGAAGAGATGTGATTTATACCTGGAAGGCC 539
DB 618 ACCAATCTGACATGCTGATGGAACATGGGGAAGAGATGTGATTTATACCTGGAAGGCC 559
QY 540 CTGGGGCAAGCAGCAATGATGCTCCATTAATGGTCCATCTCCCATCTCTGGAGATGG 599
DB 558 CTGGGGCAAGCAGCAATGATGCTCCATTAATGGTCCATCTCCCATCTCTGGAGATGG 499
QY 600 GGAAGAAAGATATGATCTTCAATCTGCTGGGCAAGAACCTGTGACGAAACTTCTCA 659
DB 498 GGAAGAAAGATATGATCTTCAATCTGCTGGGCAAGAACCTGTGACGAAACTTCTCA 439
QY 660 AGCCCATCTTCCAGAGAGCTCTGTGAAGGTGCTGATGACCAAGATTCTCCATG 719
DB 438 AGCCCATCTTCCAGAGAGCTCTGTGAAGGTGCTGATGACCAAGATTCTCCATG 379
QY 720 GTCTCTGTGTCTCTGTTGTGTCCTCTGCTGATGCTCTTTGATGAGGGCTATTT 779
DB 378 GTCTCTGTGTCTCTGTTGTGTCCTCTGCTGATGCTCTTTGATGAGGGCTATTT 319
QY 780 CTTTGTGTTCTGAAGAGAGAGACAAAGAGTATATTGAAGAAAGAGAGAGTGC 839
DB 318 CTTTGTGTTCTGAAGAGAGAGACAAAGAGTATATTGAAGAAAGAGAGAGTGC 259
QY 840 ATTGTGCGGAAATCTCTAATATGCCCCCATTTCTGAGAGAAACAGATGACACACA 899

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Db 258 ATTGTGGGAAATCTCTTAACATATGCCCCCATTTCTGGAGAGAACAGAGTACGACACA 199
QY 900 ATCCCTCACACTATAGAACCAATCTCTTAAGAGATCCAGCAATACGGTTTACTCCACT 959
Db 198 ATCCCTCACACTATAGAACCAATCTCTTAAGAGATCCAGCAATACGGTTTACTCCACT 139
QY 960 GTGGAAATACCGAAAAAGATGAAAAATCCCACTACTGCTCCAGATGCCAGACACACA 1019
Db 138 GTGGAAATACCGAAAAAGATGAAAAATCCCACTACTGCTCCAGATGCCAGACACACA 79
QY 1020 AGGCTATTTGGCCATAGATGATGTATCTAGACAGAGTCACATCCCTTAAGTCTGCTC 1079
Db 78 AGGCTATTTGGCCATAGATGATGTATCTAGACAGAGTCACATCCCTTAAGTCTGCTC 19
QY 1080 AAAAAAAAAAACA 1092
Db 18 AAAAAAAAAAAAA 6

RESULT 12
CD366342/c 749 bp mRNA linear EST 05-AUG-2004
LOCUS UI-H-FTI-b1t-g-24-0-UI.s1 NCI CGAP FTI Homo sapiens cDNA clone
DEFINITION UI-H-FTI-b1t-g-24-0-UI 3', mRNA sequence.
ACCESSION CD366342 GI:31150432
VERSION CD366342.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 749)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
DNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.iowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source Location/Qualifiers

1..749
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FTI-b1t-g-24-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="PH10B (Life Technologies)"
/clone_lib="NCI CGAP FTI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FTI is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The RNA samples
were a mixture of these conditions (lines refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The RNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,

3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldi, Lemon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCGG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-FTI
TAG_SEQ=GGCCATGCGG"

ORIGIN

Query Match 27.0%; Score 728.8; DB 6; Length 749;
Best Local Similarity 99.7%; Pred. No. 6.3e-121;
Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1307 CATAAAAAAGTGTCTTAAAGATTTCTTATGAAATGTAAATGCAGGTCCACATATTA 1366
Db 749 CATAAAAAAGTGTCTTAAAGATTTCTTATGAAATGTAAATGCAGGTCCACATATTA 690
QY 1367 ATGACAGCTGTGTATTAATGATGCTCCAGGTGAGTGTGAGTTTCAATTCATCCC 1426
Db 689 ATGACAGCTGTGTATTAATGATGCTCCAGGTGAGTGTGAGTTTCAATTCATCCC 630
QY 1427 AGGGCTTGATGTCCAGATTTATCCAGAGTCTTGCTACAGAGGAGGAGACCAAA 1486
Db 629 AGGGCTTGATGTCCAGATTTATCCAGAGTCTTGCTACAGAGGAGGAGACCAAA 570
QY 1487 ACAGACAGCAAGTCCAGACAGAGCAATGCATCTGACAAAATGATGTATTAATGGC 1546
Db 569 ACAGACAGCAAGTCCAGACAGAGCAATGCATCTGACAAAATGATGTATTAATGGC 510
QY 1547 TCTATTAATCTATGTCGCCAGACCTATGCTGAGCTTACACTAATTTGTCAGAGCTGTC 1606
Db 509 TCTATTAATCTATGTCGCCAGACCTATGCTGAGCTTACACTAATTTGTCAGAGCTGTC 450
QY 1607 TGCCCTCATGAAATTTGGCTCCAAATGAACTACTTTCAATGAGCAGTTGACAGGC 1666
Db 449 TGCCCTCATGAAATTTGGCTCCAAATGAACTACTTTCAATGAGCAGTTGACAGGC 390
QY 1667 TGACACACGATTTCCAGAGGGGTCAGGTGTGATCCACAGACTTGAAGTCAAAGTTTCAAC 1726
Db 389 TGACACACGATTTCCAGAGGGGTCAGGTGTGATCCACAGACTTGAAGTCAAAGTTTCAAC 330
QY 1727 AAAGATGAAGATCGGGTAGCTGCACATGTTGGCAGATPACTATPATGAGACACAGAA 1786
Db 329 AAAGATGAAGATCGGGTAGCTGCACATGTTGGCAGATPACTATPATGAGACACAGAA 270
QY 1787 GTGTGCATGTCGCCAAGACCAAGACCTCCAGCAGGCTTCTATTAATGACCTTGCTGCA 1846
Db 269 GTGTGCATGTCGCCAAGACCAAGACCTCCAGCAGGCTTCTATTAATGACCTTGCTGCA 210
QY 1847 AAAGAAAGTCTAGGTTTAAAGCTGTGTCAGAACCTCCCATTAAGAGACGAGTCT 1906
Db 209 AAAGAAAGTCTAGGTTTAAAGCTGTGTCAGAACCTCCCATTAAGAGACGAGTCT 150
QY 1907 GAAGTCACATTTGTAATCTAGTGTAGAGACTGTGAGTCAGGAGTGTGAGCTGGGGC 1966
Db 149 GAAGTCACATTTGTAATCTAGTGTAGAGACTGTGAGTCAGGAGTGTGAGCTGGGGC 90
QY 1967 ACGGGGGCAGTGGTACTTGTAAACCTTAAAGATGTTAATTCATTCATATGATATTT 2026
Db 89 ACGGGGGCAGTGGTACTTGTAAACCTTAAAGATGTTAATTCATTCATATGATATTT 30
QY 2027 ATTAAGAACTTA 2038

Db 29 ATTAGAACCTA 18

RESULT 13
BI767020 920 bp mRNA linear EST 25-SEP-2001
LOCUS 603054228F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5203638 5',
DEFINITION mRNA sequence.

ACCESSION BI767020
VERSION BI767020.1 GI:15758598
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 920)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L14M1510 row: h column: 07
High quality sequence stop: 743.
Location/Qualifiers

FEATURES
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1..920
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5203638"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC library."

Qy 331 AGATGATCGAGGATCTATATGTGGGGATATACAGCTCATCTCCAGACCCCTCCA 390
|
|
|
Db 301 AGATGATCGAGGATCTATATGTGGGGATATACAGCTCATCTCCAGACCCCTCCA 360
|
|
|
Qy 391 CCCAGAGTACGTGTGATGTCTTACAGAGCAGCTGTCAAGCTTAAAGTACCATGGGTC 450
|
|
|
Db 361 CCCAGAGTACGTGTGATGTCTTACAGAGCAGCTGTCAAGCTTAAAGTACCATGGGTC 420
|
|
|
Qy 451 TGCAGAGCAATTAAGATGGCACTGTGTGACCAATCTGACATCTGATGAACATGGG 510
|
|
|
Db 421 TGCAGAGCAATTAAGATGGCACTGTGTGACCAATCTGACATCTGATGAACATGGG 480
|
|
|
Qy 511 AAAGAGTGTGATTTTATCTGGAAGCCCTGGGGGAGAGAGCAATGATCCCATATG 570
|
|
|
Db 481 AAAGAGTGTGATTTTATCTGGAAGCCCTGGGGGAGAGAGCAATGATCCCATATG 540
|
|
|
Qy 571 GGTTCATCTCTCCCATCTCTGAGATGGGA-GAAAGTATGACCTTCATCTGCGTT 629
|
|
|
Db 541 GGTTCATCTCTCCCATCTCTGAGATGGGA-GAAAGTATGACCTTCATCTGCGTT 600
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|
|
Qy 630 GCCAGAACCTCTGACAGCAAACTTCTCAAGCCCATCTTGCAGAACTCTGTGA 689
|
|
|
Db 601 GCCAGAACCTCTGACAGCAAACTTCTCAAGCCCATCTTGCAGAACTCTGTGA 660
|
|
|
Qy 690 GGTGCTGTGATATACCAATTCCTCAATGTCCTCTGTCCTCTGTTGGCCCTC 749
|
|
|
Db 661 GGTGCTGTGATATACCAATTCCTCAATGTCCTCTGTCCTCTGTTGGCCCTC 720
|
|
|
Qy 750 C-TGCTCAGTCTTTTGTACTGAGGAGCTATTTCTTGTGTTCTGAAGAGAGAGA 803
|
|
|
Db 721 CTTCCTCAGTCTTTTGTACTGAGGAGCTATCTCTTGATTCGAAGAGAGAGA 775
|
|
|

RESULT 14
CD366944/c 739 bp mRNA linear EST 05-AUG-2004
LOCUS CD366944
DEFINITION UI-H-FT2-bjp-1-06-0-UI.61 NCI CGAP FT2 Homo sapiens cDNA clone
UI-H-FT2-bjp-1-06-0-UI.3, mRNA sequence.

ACCESSION CD366944
VERSION CD366944.1 GI:31151034
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 739)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers

ORIGIN

Query Match 26.7%; Score 722.2; DB 4; Length 920;
Best Local Similarity 97.4%; Pred. No. 9.2e-120;
Matches 755; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

Qy 31 CAGAGCATTATGGCTGTCCCAACAGCCCTCAACCTCATCTATATCTTTGGAGC 90
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Db 1 CAGAGCATTATGGCTGTCCCAACAGCCCTCAACCTCATCTATATCTTTGGAGC 60
|
|
|
Qy 91 TCACAGGTCAGAGCCTCTGACCCCGTGAAGAGCTGTCGTTCCGTTGGGGCCG 150
|
|
|
Db 61 TCACAGGTCAGAGCCTCTGACCCCGTGAAGAGCTGTCGTTCCGTTGGGGCCG 120
|
|
|
Qy 151 TGACTTTCCCTGAACTCAAGTAAGCAAGTTGACTTATTTCTGAGCCTTCA 210
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|
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Db 121 TGACTTTCCCTGAACTCAAGTAAGCAAGTTGACTTATTTCTGAGCCTTCA 180
|
|
|
Qy 211 CAACCCCTCTTGACCATACAGCCAGAGGGGCACTATCATATGAGACCAAAATGTA 270
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|
|
Db 181 CAACCCCTCTTGACCATACAGCCAGAGGGGCACTATCATATGAGACCAAAATGTA 240
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|
|
Qy 271 ATAGGAGAGATGATCTCCAGATGAGGCTTACTCCCTGAAAGCTCAGCAAACTGAGA 330
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Db 241 ATAGGAGAGATGATCTCCAGATGAGGCTTACTCCCTGAAAGCTCAGCAAACTGAGA 300
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FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjp-1-06-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT2"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;

NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The RNA samples were a mixture of these conditions (lines refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions). The RNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. The library was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=G3CCATGCGG"

ORIGIN

Query Match 26.5%; Score 716.4; DB 6; Length 739;

Best Local Similarity 99.2%; Pred. No. 1.1e-118;

Matches 728; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY 360 ATATACAGTCACTCACTCCAGCAGCCCTCCACCA-GAGTACGTGCTGATGCTTACGA 418
DB 739 ATATACAGTCACTCACTCCAGCAGCCCTCCACCA-GAGTACGTGCTGATGCTTACGA 680
QY 419 GCACTGTCAAAAGCCTTAAAGTCCCATGGTCTGCGAGACATTAAGATGGCCTGTGT 478
DB 679 GCACTGTCAAAAGCCTTAAAGTCCCATGGTCTGCGAGACATTAAGATGGCCTGTGT 620
QY 479 GACCAATCTGACATGTGTCATGAGAAATGGGAAAGAGATGATTTATTAACCTGGAAGG 538
DB 619 GACCAATCTGACATGTGTCATGAGAAATGGGAAAGAGATGATTTATTAACCTGGAAGG 560
QY 539 CCTGGGGCAAGCAGCAATGAGTCCCATTAATGGGTCCATCTCTCCATCTCTGAGATG 598
DB 559 CCTGGGGCAAGCAGCAATGAGTCCCATTAATGGGTCCATCTCTCCATCTCTGAGATG 500
QY 599 GGGAGAAATGATATACCTTCACTGCGTGTGCGAGAAACCTGTGACGAAATCTTTC 658
DB 499 GGGAGAAATGATATACCTTCACTGCGTGTGCGAGAAACCTGTGACGAAATCTTTC 440
QY 659 AAGCCCATCTCTGCGAGAGAGCTGTGAGAGGTGCTGATGACCCAGATTCTCCAT 718
DB 439 AAGCCCATCTCTGCGAGAGAGCTGTGAGAGGTGCTGATGACCCAGATTCTCCAT 380
QY 719 GGTCTCTCTGTGTCTCTGTGTGTCCTCTCTGCTCACTCTCTTGTACTGGGCTATT 778
DB 379 GGTCTCTCTGTGTCTCTGTGTGTCCTCTCTGCTCACTCTCTTGTACTGGGCTATT 320
QY 779 TCTTTGGTTTGAAGAGAGAGACAAAGAGTCACTTGAAGAGAGAGAGAGTGA 838
DB 319 TCTTTGGTTTGAAGAGAGAGACAAAGAGTCACTTGAAGAGAGAGAGAGTGA 260
QY 839 CATTTGTCGGGAAACTCTTAACATATGCCCCCATTTCTGAGAGAGACAGAGTACAGAC 898
DB 259 CATTTGTCGGGAAACTCTTAACATATGCCCCCATTTCTGAGAGAGACAGAGTACAGAC 200
QY 899 AATCCCTCACTAATAGAACATCTTAAAGAGATCCAGCAATACGATTACTCCAC 958
DB 199 AATCCCTCACTAATAGAACATCTTAAAGAGATCCAGCAATACGATTACTCCAC 140
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DB 139 TGTGGAATACGAAAAAGATGAAAAATCCCACTCACTGCTCAGATCCAGACACACC 80
QY 1019 AAGCATTTTGGCTTATGAGATGATTTATCTAGACAGATGACATCCCTTAATGCTCTGT 1078
DB 79 AAGCATTTTGGCTTATGAGATGATTTATCTAGACAGATGACATCCCTTAATGCTCTGT 20
QY 1079 CAAAAAAGAAAAA 1092
DB 19 CAAAAAAGAAAAA 6

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RESULT 15
CB986561 731 bp mRNA linear EST 01-MAY-2003
LOCUS AGENCOURT 13646958 NIH MGC 184 Homo sapiens cDNA clone
DEFINITION IMAGE:30327727 5', mRNA sequence.
ACCESSION CB986561
VERSION CB986561.1 GI:30281081
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 731)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gcgpb@remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLOUTech Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: NDCM137 row: d column: 08
High quality sequence stop: 599.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30327727"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 184"
/note="Torgan: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccatcgcc); Site_2: SfiI (ggcgctcgcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGGCGCCACATG-dT(30)BN-3' (where B = A,
C, or G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

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FEATURES

source

ORIGIN

Query Match 26.2%; Score 707.6; DB 6; Length 731;

Best Local Similarity 99.3%; Pred. No. 4.1e-117;

Matches 721; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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QY 14 TTTGAGTGGCTACTTCCAGAGAGCAATATGCTGCTTCCCAACATGCTTCACTCAT 73
DB 6 TTTGAGTGGCTACTTCCAGAGAGCAATATGCTGCTTCCCAACATGCTTCACTCAT 65
QY 74 CTATATCCTTTGGAGCTCAGAGGCTCGAGGCTCTGGAACCCGTAAGAGACTGGTGG 133
DB 66 CTATATCCTTTGGAGCTCAGAGGCTCGAGGCTCTGGAACCCGTAAGAGACTGGTGG 125

```

```
QY 134 TTCGTTGTGGGCGCGTGACTTTCCTCCGTAAGTCCAAAGTAAGCAAGTTGACTCTAT 193
    |||||
Db 126 TTCGTTGTGGGCGCGTGACTTTCCTCCGTAAGTCCAAAGTAAGCAAGTTGACTCTAT 185
    |||||
QY 194 TGTCTGACCTTCAACCAACCCCTCTTGTCACTATACAGCCAGAGGGGGCACTATCAT 253
    |||||
Db 186 TGTCTGACCTTCAACCAACCCCTCTTGTCACTATACAGCCAGAGGGGGCACTATCAT 245
    |||||
QY 254 AGTGACCCAAATGTATATGGGAGAGATGACTTCCAGATGAGGCTTACTCCCTGAA 313
    |||||
Db 246 AGTGACCCAAATGTATATGGGAGAGATGACTTCCAGATGAGGCTTACTCCCTGAA 305
    |||||
QY 314 GCTCAGCAAACTGAAAGAAATGACTCAGGGATCTACTATGTGGGATATACAGCTCATC 373
    |||||
Db 306 GCTCAGCAAACTGAAAGAAATGACTCAGGGATCTACTATGTGGGATATACAGCTCATC 365
    |||||
QY 374 ACTCCAGCAGCCCTCCACCCAGAGTACGTGCTCATGTCTACGAGCACCTGTCAAGCC 433
    |||||
Db 366 ACTCCAGCAGCCCTCCACCCAGAGTACGTGCTCATGTCTACGAGCACCTGTCAAGCC 425
    |||||
QY 434 TAAAGTACCATGGGTCTGCAAGACATTAAGAAATGGCACTGTGTGACCAATCTGACATG 493
    |||||
Db 426 TAAAGTACCATGGGTCTGCAAGACATTAAGAAATGGCACTGTGTGACCAATCTGACATG 485
    |||||
QY 494 CTGCATGGAACATGGGGAAGAGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGC 553
    |||||
Db 486 CTGCATGGAACATGGGGAAGAGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGC 545
    |||||
QY 554 CAATGAGTCCCATTAATGGGTCCATCTCCCATCTCTGAGATGGGGAAGAAAGTATAT 613
    |||||
Db 546 CAATGAGTCCCATTAATGGGTCCATCTCCCATCTCTGAGATGGGGAAGAAAGTATAT 605
    |||||
QY 614 GACCTTCATCTGCGTGTGCGCAGAAACCTGTGACGAGAACTTCTCAAGCCCATCTTGC 673
    |||||
Db 606 GACCTTCATCTGCGTGTGCGCAGAAACCTGTGACGAGAACTTCTCAAGCCCATCTTGC 665
    |||||
QY 674 CAGGAAGCTCTGTGAAGTGTGCTGATGACCCAGATTCTCATGGT-CCTCCTGTGTC 732
    |||||
Db 666 CAGGAAGCTCTGTGAAGTGTGCTGATGACCCAGAAITCTCATGGTCCCTCCTGTGTC 725
    |||||
QY 733 TCCTGT 738
    |||||
Db 726 TCCTGT 731
```

Search completed: October 28, 2004, 10:16:56
Job time : 8258 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 03:09:04 ; Search time 1275 Seconds
(without alignments)
11132.890 Million cell updates/sec

Title: US-09-745-605-1

Perfect score: 2704

Sequence: 1 ggaagtcgtcattcattcagc.....aaaaaaaaaaaaaaaaaaaa 2704

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: geneseqn1980s:*\n2: geneseqn1990s:*\n3: geneseqn2000s:*\n4: geneseqn2001s:*\n5: geneseqn2001bs:*\n6: geneseqn2002as:*\n7: geneseqn2002bs:*\n8: geneseqn2003as:*\n9: geneseqn2003bs:*\n10: geneseqn2003cs:*\n11: geneseqn2003ds:*\n12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2704	100.0	2704	5	AAC86114
2	2617.2	96.8	2774	3	AAC55192
3	2604.6	96.3	2672	10	ADD67524
4	2186.4	80.9	2780	3	AAC55223
5	1728.8	63.9	3651	12	ADQ24216
6	1369.4	50.6	1412	2	AAX00615
7	1369.4	50.6	1412	3	AAC55224
8	1369.4	50.6	1412	8	ADA40261
9	1369.4	50.6	1412	10	ADA56425
10	1256.6	46.5	1272	3	AAS51572
11	1082	40.0	1082	8	ACCT72129
12	1076	39.8	1076	3	AAZ65040
13	1076	39.8	1076	4	AAAS4620
14	1076	39.8	1076	4	AAAF92080
15	1076	39.8	1076	5	AAAF44186
16	1076	39.8	1076	6	ABE74400
17	1076	39.8	1076	8	ACA89470
18	1076	39.8	1076	8	ACA73480
19	1076	39.8	1076	8	ACA05795
20	1076	39.8	1076	8	ACA66629
21	1076	39.8	1076	8	ACA64332

22	1076	39.8	1076	8	ACA91186	ACA91186	Novel	hum
23	1076	39.8	1076	8	ACD81563	ACD81563	Human	CDN
24	1076	39.8	1076	8	ACF20204	ACF20204	Human	sec
25	1076	39.8	1076	8	ACF19590	ACF19590	Human	sec
26	1076	39.8	1076	8	ACD21878	ACD21878	Human	sec
27	1076	39.8	1076	8	ACF13043	ACF13043	Human	sec
28	1076	39.8	1076	8	ACD25146	ACD25146	Human	sec
29	1076	39.8	1076	8	ACF00195	ACF00195	Human	sec
30	1076	39.8	1076	8	ACA60385	ACA60385	Novel	hum
31	1076	39.8	1076	8	ACA72252	ACA72252	Novel	hum
32	1076	39.8	1076	8	ACD04776	ACD04776	Novel	hum
33	1076	39.8	1076	8	ACD18237	ACD18237	Human	sec
34	1076	39.8	1076	8	ACD08244	ACD08244	Human	sec
35	1076	39.8	1076	8	ACA86678	ACA86678	Novel	hum
36	1076	39.8	1076	8	ACA70120	ACA70120	Human	sec
37	1076	39.8	1076	8	ACD12342	ACD12342	Novel	hum
38	1076	39.8	1076	8	ACCT4257	ACCT4257	Human	sec
39	1076	39.8	1076	8	ACD15885	ACD15885	Human	sec
40	1076	39.8	1076	8	ACD25453	ACD25453	Novel	hum
41	1076	39.8	1076	8	ACD17930	ACD17930	Human	sec
42	1076	39.8	1076	8	ACC88217	ACC88217	Human	sec
43	1076	39.8	1076	8	ACD1571	ACD1571	Human	sec
44	1076	39.8	1076	8	ACD18638	ACD18638	Human	sec
45	1076	39.8	1076	8	ACA58832	ACA58832	CDNA	enco

ALIGNMENTS

RESULT 1	
AAC86114	
ID	AAC86114 standard; CDNA; 2704 BP.
XX	
AC	AAC86114;
XX	
DT	29-AUG-2001 (first entry)
XX	
DE	APEX-1 CDNA.
XX	
KW	Antigen presenting cell expression protein; APEX-1; APEX-2; APEX-3;
KW	extracellular domain; immunoglobulin-like domain; Ig-like structure;
KW	N-glycosylation site; transmembrane domain; cytoplasmic domain;
KW	SH2-binding motif; ashma; arteriosclerosis; AIDS; cirrhosis;
KW	Crohn's disease; atopic dermatitis; autoimmune anaemia; bursitis;
KW	cholecystitis; diabetes mellitus; emphysema; atrophic gastritis;
KW	inflammatory bowel disease; multiple sclerosis; myasthenia gravis;
KW	myocardial infarction; pericardial inflammation; osteoarthritis;
KW	osteoporosis; psoriasis; Reiter's syndrome; rheumatoid arthritis;
KW	inflammation; cancer; autoimmune disease; graft rejection;
KW	graft versus host disease; systemic lupus erythematosus; se.
XX	
OS	Homo sapiens.
XX	
XX	
Key	Location/Qualifiers
FT	CD5 42..1049
FT	/*tag= a
FT	/product= "APEX-1"
FT	sig_peptide 42..107
FT	/*tag= b
FT	mat_peptide 108..1046
FT	/*tag= c
XX	
PN	W0200146260-A2.
XX	
XX	
PD	28-JUN-2001.
XX	
PF	22-DEC-2000; 2000MO-US034963.
XX	
PR	23-DEC-1999; 99US-0172025P.
XX	
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.
XX	
PI	Starling GC, Finger J;

XX MPI; 2001-418044/44.
DR P-PSDB; AAB47321.
XX
PT Novel Antigen Presenting cell expression protein useful for treating
PT asthma, arteriosclerosis, autoimmune diseases, AIDS, cirrhosis, Crohn's
PT disease and atopic dermatitis.
XX
PS Claim 2; Fig 2; 112pp; English.
XX

CC The sequences given in AAC8614-16 encode antigen presenting cell
CC expression (APEX)-1, APEX-2 and APEX-3 proteins. APEX-1 and APEX-2
CC comprise an extracellular domain having one immunoglobulin (Ig)-like
CC structure and N-glycosylation site, a transmembrane domain, and a
CC cytoplasmic domain having at least one SH2-binding motif. APEX proteins
CC and antibodies are useful in the study, diagnosis, prevention and
CC treatment of disease associated with the presence of an APEX protein
CC e.g., asthma, arteriosclerosis, AIDS, cirrhosis, Crohn's disease, atopic
CC dermatitis, autoimmune anaemia, bursitis, cholecystitis, diabetes
CC mellitus, emphysema, atrophic gastritis, inflammatory bowel disease,
CC multiple sclerosis, myasthenia gravis, myocardial or pericardial
CC inflammation, osteoarthritis, osteoporosis, psoriasis, Reiter's syndrome,
CC rheumatoid arthritis, inflammation, cancer, immune disorders, autoimmune
CC diseases, graft rejections, graft versus host reaction and systemic lupus
CC erythematosus. APEX proteins are useful as diagnostic and/or prognostic
CC markers on APCs or APEX expressing cells, the ability to elicit the
CC generation of antibodies and as targets for various therapeutic
CC modalities. APEX proteins are also useful for identifying and isolating
CC ligand that bind APEX

XX Sequence 2704 BP; 824 A; 618 C; 629 G; 633 T; 0 U; 0 Other;

Query Match 100.0%; Score 2704; DB 5; Length 2704;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2704; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGTGCTTCAATTCAGTGGCTGACTTCAGAGAGCAATATGCTGTTCCCAACAT 60
DB 1 GGAAGTGCTTCAATTCAGTGGCTGACTTCAGAGAGCAATATGCTGTTCCCAACAT 60
QY 61 GCTTCACTCATCTATCTATCTTGGAGCTGACAGGGTCAGAGAGCTTGGACCCGTGA 120
DB 61 GCTTCACTCATCTATCTATCTTGGAGCTGACAGGGTCAGAGAGCTTGGACCCGTGA 120
QY 121 AAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
DB 121 AAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
QY 181 AAGTGAATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 240
DB 181 AAGTGAATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 240
QY 241 GGGGCACTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 300
DB 241 GGGGCACTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 300
QY 301 GCTACTCCCTGAAGCTCAGCAAACTGAAGAAGATGCTCAGGGATCTATGTTGGGA 360
DB 301 GCTACTCCCTGAAGCTCAGCAAACTGAAGAAGATGCTCAGGGATCTATGTTGGGA 360
QY 361 TATACAGCTCATCTACCTCAGAGAGCTTCAAGAGATGCTGCTCATGTTCTACGAGC 420
DB 361 TATACAGCTCATCTACCTCAGAGAGCTTCAAGAGATGCTGCTCATGTTCTACGAGC 420
QY 421 ACCCTGCAAGCCTTAAGTCAACATGGGTCTGAGAGCAATAAGATGGCACTGTGTGA 480
DB 421 ACCCTGCAAGCCTTAAGTCAACATGGGTCTGAGAGCAATAAGATGGCACTGTGTGA 480
QY 481 CCAATCTGACATGCTCATGGAACATGGGGAGAAGATGATGATTTATCTGGGAAGCCC 540
DB 481 CCAATCTGACATGCTCATGGAACATGGGGAGAAGATGATGATTTATCTGGGAAGCCC 540
QY 541 TGGGCAAGCAAGCAATGAGTCCCATATGAGTCCATCTCCCATCTCTGGAGATGGG 600

DB 541 TGGGCAAGCAAGCAATGAGTCCCATATGAGTCCCATCTCTCTGGAGATGGG 600
QY 601 GAGAAAGATATGACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 GAGAAAGATATGACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 GCCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 GCCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 TTTGGTTTCTGAAG 840
DB 781 TTTGGTTTCTGAAG 840
QY 841 TTTGGTTTCTGAAG 900
DB 841 TTTGGTTTCTGAAG 900
QY 901 TCCCTCACTATATGAAACAATCTTAAAGAGATCCAGAAATACGGTTTACTCCACTG 960
DB 901 TCCCTCACTATATGAAACAATCTTAAAGAGATCCAGAAATACGGTTTACTCCACTG 960
QY 961 TGGAAATCCGAAAG 1020
DB 961 TGGAAATCCGAAAG 1020
QY 1021 GCTATTTTCTGATGAGATGTTATCTAGACAGAGTGCATCCCTTAAGTCTGCTCA 1080
DB 1021 GCTATTTTCTGATGAGATGTTATCTAGACAGAGTGCATCCCTTAAGTCTGCTCA 1080
QY 1081 AAAAAAAACAATTTCTGGCCCAAGAAACAATCAGAAATTCAGATTTGACTGAGA 1140
DB 1081 AAAAAAAACAATTTCTGGCCCAAGAAACAATCAGAAATTCAGATTTGACTGAGA 1140
QY 1141 AACATCAAG 1200
DB 1141 AACATCAAG 1200
QY 1201 CTTTGAATTTAAGATGTTGTAATTCATCTCAGTGAAGATCTCTCAAAACCAAGAG 1260
DB 1201 CTTTGAATTTAAGATGTTGTAATTCATCTCAGTGAAGATCTCTCAAAACCAAGAG 1260
QY 1261 GTTTAATCACTTCAATCCAAAGATGGAATGTCAGCAACATTAAGAGAGAGAGAG 1320
DB 1261 GTTTAATCACTTCAATCCAAAGATGGAATGTCAGCAACATTAAGAGAGAGAGAG 1320
QY 1321 TTAAGAGATTCCTTATAGAAATGTAATGCAAGGTCACACATTAATTAAGAGAGAG 1380
DB 1321 TTAAGAGATTCCTTATAGAAATGTAATGCAAGGTCACACATTAATTAAGAGAGAG 1380
QY 1381 TATTAATGATGCTCAGGTGATGCTGAGTTCATTCATCCAGAGGCTTGATGTC 1440
DB 1381 TATTAATGATGCTCAGGTGATGCTGAGTTCATTCATCCAGAGGCTTGATGTC 1440
QY 1441 AGGATTAATCAAGAGTCTTGTCTACAGAGGGCAAGAACCAAAACAGACAGCAAGT 1500
DB 1441 AGGATTAATCAAGAGTCTTGTCTACAGAGGGCAAGAACCAAAACAGACAGCAAGT 1500
QY 1501 CCAG 1560
DB 1501 CCAG 1560
QY 1561 GCCCAGACATATGCTGAGCTTACATTAATGCTGAGAGAGAGAGAGAGAGAGAGAG 1620
DB 1561 GCCCAGACATATGCTGAGCTTACATTAATGCTGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 TGGCTCAATGATGAATCTATCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680

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Db      1621 TGCGTCCAAATGAATGAATGAACTACTTTCATGACGAGTGTGAGCAGGCGTCGACACAGATTC 1680
Qy      1681 CAGAGGGCGAGGTGTGATCCACAGACTTGAAGTCAAATTCACAAAGTGAAGATC 1740
Db      1681 CAGAGGGCGAGGTGTGATCCACAGACTTGAAGTCAAATTCACAAAGTGAAGATC 1740
Qy      1741 AGGGTAGCTGACCATGTTTGGCAGATTAATATGAGAGACAGAGAGTGCATGGCCCA 1800
Db      1741 AGGGTAGCTGACCATGTTTGGCAGATTAATATGAGAGACAGAGAGTGCATGGCCCA 1800
Qy      1801 AGGACAGAGACCTTCAGCCAGGCTTCATTATGACCTTGCTGCAAAAAGAAAGTCTAG 1860
Db      1801 AGGACAGAGACCTTCAGCCAGGCTTCATTATGACCTTGCTGCAAAAAGAAAGTCTAG 1860
Qy      1861 GTTTTAAAGCTGTGCGCAGAACCCATCCCAATAAAGAGCCAGTCTGAAATGACATTGTA 1920
Db      1861 GTTTTAAAGCTGTGCGCAGAACCCATCCCAATAAAGAGCCAGTCTGAAATGACATTGTA 1920
Qy      1921 AATCTAGTGTAGAGACTTGGAGTCAAGGACGTGAGACTGCTGCTGGGGCAGGGGGCAGTGG 1980
Db      1921 AATCTAGTGTAGAGACTTGGAGTCAAGGACGTGAGACTGCTGCTGGGGCAGGGGGCAGTGG 1980
Qy      1981 GTACTTGTAAACCTTTAAAGATGATTAATTCATTCAATAGATTTTATTAAGAACTACT 2040
Db      1981 GTACTTGTAAACCTTTAAAGATGATTAATTCATTCAATAGATTTTATTAAGAACTACT 2040
Qy      2041 ATGGGGCCCCGATGAGTGTGCTCACAACCTGTAAATCCAGACTTTTGGAGGCGCAAGTGGG 2100
Db      2041 ATGGGGCCCCGATGAGTGTGCTCACAACCTGTAAATCCAGACTTTTGGAGGCGCAAGTGGG 2100
Qy      2101 TGGGTCACTGAGGCTCAGAGAGTTCAAGACAGCCCTGGGCAACATGTAAGAAACCCCATCTC 2160
Db      2101 TGGGTCACTGAGGCTCAGAGAGTTCAAGACAGCCCTGGGCAACATGTAAGAAACCCCATCTC 2160
Qy      2161 TACTAAAGATCAAAATTTGCTGAGCGTGTGTGTGTGCACTGTATCCAGCTACTCGAGA 2220
Db      2161 TACTAAAGATCAAAATTTGCTGAGCGTGTGTGTGTGTGCACTGTATCCAGCTACTCGAGA 2220
Qy      2221 GGGCAAGGCGATGAGAAATGCTTGAACCTGAGAGTGTGAGTTCAGTGAAGTGGCAC 2280
Db      2221 GGGCAAGGCGATGAGAAATGCTTGAACCTGAGAGTGTGAGTTCAGTGAAGTGGCAC 2280
Qy      2281 CACTGCACTCGGCGCTTGGGCAAGAGCAAAATCCCAATGCAAAACAAACAAACAC 2340
Db      2281 CACTGCACTCGGCGCTTGGGCAAGAGCAAAATCCCAATGCAAAACAAACAAACAC 2340
Qy      2341 CTGTGCTAGGTCACTGTGCGACGTAAATGTAATCCCTACCAACAGAGCTCAGCATC 2400
Db      2341 CTGTGCTAGGTCACTGTGCGACGTAAATGTAATCCCTACCAACAGAGCTCAGCATC 2400
Qy      2401 TCTTATTACTTAAGTGAAGAAACATGAGGAGGGAAGGGGAAATGCTGCTTTGATATGT 2460
Db      2401 TCTTATTACTTAAGTGAAGAAACATGAGGAGGGAAGGGGAAATGCTGCTTTGATATGT 2460
Qy      2461 TCCCTGACGATATCTTGAATGAGACCTCCCTCAACAGATGATAAGTGTGAAAAACT 2520
Db      2461 TCCCTGACGATATCTTGAATGAGACCTCCCTCAACAGATGATAAGTGTGAAAAACT 2520
Qy      2521 TAATTAACAAATGCTTGTGGGCAAGAAATGGAATTTATCTTCTCAGAAAAAGCA 2580
Db      2521 TAATTAACAAATGCTTGTGGGCAAGAAATGGAATTTATCTTCTCAGAAAAAGCA 2580
Qy      2581 TTGTGAAGGAATTAAGCCAGATCTCTCTCCTTACTGCAAAAACCTTATTTGTAAGAAAG 2640
Db      2581 TTGTGAAGGAATTAAGCCAGATCTCTCTCCTTACTGCAAAAACCTTATTTGTAAGAAAG 2640
Qy      2641 TCTCTTAACTATCTTATATAAACAGATATTTGAGATTCAATAAAAAAGAAAAA 2700
Db      2641 TCTCTTAACTATCTTATATAAACAGATATTTGAGATTCAATAAAAAAGAAAAA 2700
Qy      2701 AAAA 2704
Db      2701 AAAA 2704

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RESULT 2
AAC55192
ID AAC55192 standard; cDNA; 2774 BP.
XX
AC AAC55192;
XX
DT 16-JAN-2001 (first entry)
XX
DE Human secreted protein gene 3 SEQ ID NO:13.
XX
KW Human; secreted protein; cytosolic; immunostimulant; antiproliferative;
KW cardiant; antiarrhythmic; antiviral; antibacterial; antifungal; cancer;
KW antiparasitic; neuroprotective; nootropic; antiinflammatory; anti-HIV;
KW antiangiogenic; antiarteriosclerotic; diagnosis; immune disorder; AIDS;
KW autoimmune disease; haematopoietic cell disorder; blood protein disorder;
KW agammaglobulinaemia; hyperproliferative disease; Gaucher's disease;
KW cardiovascular disorder; congenital heart defect; pulmonary atresia;
KW arrhythmia; ischaemia; angiogenesis related disorder; Crohn's disease;
KW atherosclerosis; neurological disease; Alzheimer's disease; Huntington's;
KW infectious disease; cat-scratch disease; chromosome 1; ss.
XX
OS Homo sapiens.
XX
PN M0200047602-A1.
XX
PD 17-AUG-2000.
XX
PF 08-FEB-2000; 2000MO-US003062.
XX
PR 10-FEB-1999; 99US-0119468P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Young PE, Ni J, Soppet DR;
PI Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence KA, Komatsuouli G;
XX
DR WPI; 2000-543578/49.
XX
PT P-PSDB; AAB32373.
XX
PT New human nucleic acids encoding secreted proteins, useful in the
PT treatment, prevention or diagnosis of immune disorders (e.g. autoimmune
PT diseases), blood protein disorders and hyperproliferative diseases (e.g.
PT Gaucher's disease).
XX
PS Claim 1; Page 392-393; 488pp; English.
XX
CC The polynucleotide sequences given in AAC55190 to AAC55235 encode the
CC human secreted proteins given in AAB32371 to AAB32484. Human secreted
CC proteins have activities based on the tissues and cells the genes are
CC expressed in. Examples of activities include: cytosolic; immunostimulant
CC ; antiproliferative; cardiant; antiarrhythmic; antiviral; antibacterial;
CC antifungal; antiparasitic; neuroprotective; nootropic; antiinflammatory;
CC antiangiogenic; anti-HIV; and antiarteriosclerotic. The polynucleotides
CC and polypeptides, or their agonists and antagonists, can be used for
CC treating, preventing or diagnosing immune disorders (e.g. cancer,
CC autoimmune diseases), disorders of haematopoietic cells, blood protein
CC disorders (e.g. agammaglobulinaemia), hyperproliferative diseases (e.g.
CC Gaucher's disease), cardiovascular disorders (e.g. congenital heart
CC defects, pulmonary atresia, arrhythmias, ischaemia), angiogenesis related
CC disorders (e.g. Crohn's disease, atherosclerosis), neurological diseases
CC (e.g. Alzheimer's disease, Huntington's chorea), infectious diseases
CC (e.g. AIDS, cat-scratch disease and other bacterial, viral, parasitic or
CC fungal diseases). AAC55181 to AAC55189 and AAB32370 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 2774 BP; 841 A; 632 C; 645 G; 644 T; 0 U; 12 Other;

```

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Query Match 96.8%; Score 2617.2; DB 3; Length 2774;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2669; Conservative 6; Mismatches 22; Indels 7; Gaps 4;

```


QY 1 GGAAGTGGCTTCATTTCACTGAGTGGCTTCAGAGAGCAATATGGCTGGTTCCCAACAT 60
| | | | |
Db 13 GGAAGTGGCTTCATTTCACTGAGTGGCTTCAGAGAGCAATATGGCTGGTTCCCAACAT 72
| | | | |
QY 61 GCCTCAACCTCATCTATATCTTTGGCAGCTCAAGGCTAGAGCTCTGGACCCGTGA 120
| | | | |
Db 73 GCCTCAACCTCATCTATATCTTTGGCAGCTCAAGGCTAGAGCTCTGGACCCGTGA 132
| | | | |
QY 121 AAGAGTGGTGGCTTCGTTGGTGGGCGTGACTTTCCCTGGAAGTCCAAAGTAAAG 180
| | | | |
Db 133 AAGAGTGGTGGCTTCGTTGGTGGGCGTGACTTTCCCTGGAAGTCCAAAGTAAAG 192
| | | | |
QY 181 AAGTTACTCTATTTGTCTGAGCTTCAACAACCCCTCTTGTACCATACAGCCAGAAG 240
| | | | |
Db 193 AAGTTACTCTATTTGTCTGAGCTTCAACAACCCCTCTTGTACCATACAGCCAGAAG 252
| | | | |
QY 241 GGGGCACTATCATAGTGAACCAAAATCTGTAATGGAGAGAGTGAATTTCCCGATGGAG 300
| | | | |
Db 253 GGGGCACTATCATAGTGAACCAAAATCTGTAATGGAGAGAGTGAATTTCCCGATGGAG 312
| | | | |
QY 301 GCTACTCCCTGAGCTCAGCAAACTGAAGAAGATGCTCAGGGATCTACTATGTGGGA 360
| | | | |
Db 313 GCTACTCCCTGAGCTCAGCAAACTGAAGAAGATGCTCAGGGATCTACTATGTGGGA 372
| | | | |
QY 361 TATACAGCTCATCTCCAGCAGCCCTCCACCCAGAGATACGTGCTGATGTACAGC 420
| | | | |
Db 373 TATACAGCTCATCTCCAGCAGCCCTCCACCCAGAGATACGTGCTGATGTACAGC 432
| | | | |
QY 421 ACCTGCAAAAGCCTTAAGTCAACATGGGTCTGAGAGCAATTAAGATGGACCTGTGTGA 480
| | | | |
Db 433 ACCTGCAAAAGCCTTAAGTCAACATGGGTCTGAGAGCAATTAAGATGGACCTGTGTGA 492
| | | | |
QY 481 CCAATCTGACATGCTGCATAGGAACATGGGGAAGAGATGATTTATCTGGAAGGCC 540
| | | | |
Db 493 CCAATCTGACATGCTGCATAGGAACATGGGGAAGAGATGATTTATCTGGAAGGCC 552
| | | | |
QY 541 TGGGGCAAGCAGCAATGAGTCCCATATAGGTCCATCTCTCCCATCTCTGAGATGG 600
| | | | |
Db 553 TGGGGCAAGCAGCAATGAGTCCCATATAGGTCCATCTCTCCCATCTCTGAGATGG 612
| | | | |
QY 601 GAGAAGTGAATAGACCTTCATCTGGTGGCAGGAACCTTCACAGAGAAATTTCTCA 660
| | | | |
Db 613 GAGAAGTGAATAGACCTTCATCTGGTGGCAGGAACCTTCACAGAGAAATTTCTCA 672
| | | | |
QY 661 GCCCCTCTCTGCGCAGGAAGCTCTGGAAGTCTGCTGATGACCCAGATTCCTCCATG 720
| | | | |
Db 673 GCCCCTCTCTGCGCAGGAAGCTCTGGAAGTCTGCTGATGACCCAGATTCCTCCATG 732
| | | | |
QY 721 TCTCTCTGTGTCTCTGTGTGTGTCCTCTCTGCTCAAGTCTCTTGTATCTGGGGCTATTT 780
| | | | |
Db 733 TCTCTCTGTGTCTCTGTGTGTGTCCTCTCTGCTCAAGTCTCTTGTATCTGGGGCTATTT 792
| | | | |
QY 781 TTTGTGTTCTGAAGAGAGAGAGCAAGAGAGTACATTGAAGAGAGAGAGTGTGACA 840
| | | | |
Db 793 TTTGTGTTCTGAAGAGAGAGAGCAAGAGAGTACATTGAAGAGAGAGAGTGTGACA 852
| | | | |
QY 841 TTTGTGCGGAATCTCTTAATATGCCCCATCTGGAAGAACACAGAGTACAGACAA 900
| | | | |
Db 853 TTTGTGCGGAATCTCTTAATATGCCCCATCTGGAAGAACACAGAGTACAGACAA 912
| | | | |
QY 901 TCCCTCACTAATAAGAACATCTTAAGAGAGATCAGCAAAATACGGTTTACTCCAGTG 960
| | | | |
Db 913 TCCCTCACTAATAAGAACATCTTAAGAGAGATCAGCAAAATACGGTTTACTCCAGTG 972
| | | | |
QY 961 TGGAAATACCGAAAGAGTGAAGATCCCACTCATCTGCTCAGAGATCCAGACACCAA 1020
| | | | |
Db 973 TGGAAATACCGAAAGAGTGAAGATCCCACTCATCTGCTCAGAGATCCAGACACCAA 1032
| | | | |
QY 1021 GGGTATTTTGTGAGAAATGTTATCTAGACAGCAGTGCATCCCTAAGTCTCTGCTCA 1080
| | | | |
Db 1033 GGGTATTTTGTGAGAAATGTTATCTAGACAGCAGTGCATCCCTAAGTCTCTGCTCA 1092
| | | | |
QY 1081 AAAAAAACAATTTCTGGGCCCAAGAAAAAATCAATCAGAAATTCATGATTTGACTAGA 1140
| | | | |

Db 1093 AAAAAAACAATTTCTGGGCCCAAGAAAAAATCAATCAGAAATTCATGATTTGACTAGA 1152
| | | | |
QY 1141 AACATCAAGAGAGATGAAGAACGTGACTTTTTTCCAGAGTAATTTATCTGTATGCT 1200
| | | | |
Db 1153 AACATCAAGAGAGATGAAGAACGTGACTTTTTTCCAGAGTAATTTATCTGTATGCT 1212
| | | | |
QY 1201 CTTTAGATTTAAGATTCGTAAATTCATCCATGCTGAGAAATCTCTCAAAACAGAG 1260
| | | | |
Db 1213 CTTTAGATTTAAGATTCGTAAATTCATCCATGCTGAGAAATCTCTCAAAACAGAG 1272
| | | | |
QY 1261 GTTTAATCATCTTCATCCAAAAATGGATTTGAATGTCAGCAACATAAAAAATGTC 1320
| | | | |
Db 1273 GTTTAATCATCTTCATCCAAAAATGGATTTGAATGTCAGCAACATAAAAAATGTC 1332
| | | | |
QY 1321 TTAGAAGTTCCTTATAGAAATGTAATGCAAGTCAACATATTAATGACAGCCGTGG 1380
| | | | |
Db 1333 TTAGAAGTTCCTTATAGAAATGTAATGCAAGTCAACATATTAATGACAGCCGTGG 1392
| | | | |
QY 1381 TATTAATGATGGCTCCAGGTCAGTCTGAGATTCATTCATCCAGGGCTTGGATGTC 1440
| | | | |
Db 1393 TATTAATGATGGCTCCAGGTCAGTCTGAGATTCATTCATCCAGGGCTTGGATGTC 1452
| | | | |
QY 1441 AGGATTTATCCAAAGTCTTGTCTACCAAGAGGCAAGAACCAAAACAGACACAACT 1500
| | | | |
Db 1453 AGGATTTATCCAAAGTCTTGTCTACCAAGAGGCAAGAACCAAAACAGACACAACT 1512
| | | | |
QY 1501 CAGAGCAAGCAGATGACCTGACAAAAATGATATTAATTTGGCTCATATAATGT 1560
| | | | |
Db 1513 CAGAGCAAGCAGATGACCTGACAAAAATGATATTAATTTGGCTCATATAATGT 1572
| | | | |
QY 1561 GCCCAGCATATGCTGAGCTTACACTAAATGGTCCAGAGTGTCTGCTCCATGAAAT 1620
| | | | |
Db 1573 GCCCAGCATATGCTGAGCTTACACTAAATGGTCCAGAGTGTCTGCTCCATGAAAT 1632
| | | | |
QY 1621 TGGCTCCAAATGAATGAATCTATTTCTAGAGAGTTTGAAGAGGCTGACCAAGATTC 1680
| | | | |
Db 1633 TGGCTCCAAATGAATGAATCTATTTCTAGAGAGTTTGAAGAGGCTGACCAAGATTC 1692
| | | | |
QY 1681 CAGAGGGCCAGGTGATGATCCACAGAGCTTGAAGGTCAAAGTTCACAAAGATGAATTC 1740
| | | | |
Db 1693 CAGAGGGCCAGGTGATGATCCACAGAGCTTGAAGGTCAAAGTTCACAAAGATGAATTC 1752
| | | | |
QY 1741 AGGATAGCTGACCAATGTTTGGCAGATACATATATGAGACACAGAGTGTGATGGCCA 1800
| | | | |
Db 1753 AGGATAGCTGACCAATGTTTGGCAGATACATATATGAGACACAGAGTGTGATGGCCA 1812
| | | | |
QY 1801 AGGACAGGACCTCCAGCCAGGCTTCAATTTATGCACTTGTGCTGCAAAAAAGTCTAG 1860
| | | | |
Db 1813 AGGACAGGACCTCCAGCCAGGCTTCAATTTATGCACTTGTGCTGCAAAAAAGTCTAG 1872
| | | | |
QY 1861 GTTTAAAGCTGTGCAGAACCATCCCAATTAAGACCGAGTGTGAAGTCAATTTGA 1920
| | | | |
Db 1873 GTTTAAAGCTGTGCAGAACCATCCCAATTAAGACCGAGTGTGAAGTCAATTTGA 1932
| | | | |
QY 1921 AATCTAGTGAAGACTTGAAGTCAAGGACAGTGAAGTGTGGGCAAGGGGGCAGTGG 1980
| | | | |
Db 1933 AATCTAGTGAAGACTTGAAGTCAAGGACAGTGAAGTGTGGGCAAGGGGGCAGTGG 1992
| | | | |
QY 1981 GTACTTGTAACTTTTAAAGATGTTAATTTCAATAGATATTTAATTAAGACTTACT 2040
| | | | |
Db 1993 GTACTTGTAACTTTTAAAGATGTTAATTTCAATAGATATTTAATTAAGACTTACT 2049
| | | | |
QY 2041 ATGGGGCCCGGATGGTGTGACACCTGTATATCCAGACTTTGGAGGCGCAAGTGGG 2100
| | | | |
Db 2050 ATGGGGCCCGGATGGTGTGACACCTGTATATCCAGACTTTGGAGGCGCAAGTGGG 2109
| | | | |
QY 2101 TGGGTCACTGAGGTCAAGAGTTTCAAGACAGCCTGCGCAACATGTTGAATCC-CATCT 2159
| | | | |
Db 2110 TGGGTCACTGAGGTCAAGAGTTTCAAGACAGCCTGCGCAACATGTTGAATCCCACTCT 2169
| | | | |
QY 2160 CTACTAAGATCAAAATTTGCTGAGCGTGTGTGTGACCTGT-ATCCAGCTACTGCA 2218
| | | | |

Db	2170	ACTAAGATACAAAAATTTGCTGAGCGGTGTGTGTGACACTGTAAATCCACGTA	222	229
Oy	2219	GAGGCCAAGGCATGAGAAATCGCTTGAACCTGG--AGTGAAGTGGTCACTGAGTGAATG	227	234
Db	2230	GAGGCCAAGGCATGAGAAATCGCTTGAACCTGGAGAGTGAAGGTTCAGTGAAGTGAATG	228	235
Oy	2277	GCACCACTGCACCTCCGGCTTGGGCAAGAGAGCAAAATCTCCAAATCAAAACAAACAA	233	240
Db	2290	GCACCACTGCACCTCCGGCTTGGGCAAGAGAGCAAAATCTCCAAATCAAAACAAACAA	234	241
Oy	2337	ACACCTGTGCTAGGTCACTGTGGCAGCTAAGATGAACATCCCTACCAACAGAGCTCAC	239	246
Db	2350	ACACCTGTGCTAGGTCACTGTGGCAGCTAAGATGAACATCCCTACCAACAGAGCTCAC	240	247
Oy	2397	CATCTCTTATATCTTAAGTAAAAACATGGGGAAGGGGAAGGGGAATGGCTGCTTTGAT	245	252
Db	2410	CATCTCTTATATCTTAAGTAAAAACATGGGGAAGGGGAAGGGGAATGGCTGCTTTGAT	246	253
Oy	2457	ATGTTTCCCTGACGCATATCTTGAATGAGACCTCCTACCAAGTATGAAGTGTGAAA	251	258
Db	2470	ATGTTTCCCTGACGCATATCTTGAATGAGACCTCCTACCAAGTATGAAGTGTGAAA	252	259
Oy	2517	AACTTAATAAACAAATGCTTGTGGCAGAAATGGATGGAGATTAATCTTCTCAGAAA	257	264
Db	2530	AACTTAATAAACAAATGCTTGTGGCAGAAATGGATGGAGATTAATCTTCTCAGAAA	258	265
Oy	2577	GGCATTTGGAAGAAATTGAGCCAGATCTCTCTCCTACTGCAAAACCTATTTGATGAA	263	270
Db	2590	GGCATTTGGAAGAAATTGAGCCAGATCTCTCTCCTACTGCAAAACCTATTTGATGAA	264	271
Oy	2637	AAAGCTTCTTTATCTATCTTAAATAAACAATTTGAGATTCAATAAAAA	269	276
Db	2650	AAAGCTTCTTTATCTATCTTAAATAAACAATTTGAGATTCAATTTCTTCAGAAA	270	277
Oy	2697	AAAA 2700		
Db	2710	AAAA 2713		
RESULT 3				
ADD67524				
ID	ADD67524	standard; cDNA, 2672 BP.		
XX	ADD67524;			
XX	15-JAN-2004	(first entry)		
DE	Human Lyr1728P encoding cDNA SEQ ID NO:1.			
XX	haematological malignancy; immunocytoma; cytostatic; immunosuppressant;			
KW	haematological malignancy; immunocytoma; cancer; multiple myeloma cell;			
KW	chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;			
XX	human; gene; 88.			
OS	Homo sapiens.			
XX	MO2003062401-A2.			
XX	31-JUL-2003.			
XX	22-JAN-2003; 2003WO-US002353.			
PF	22-JAN-2002; 2002US-00057475.			
XX	(CORI-) CORIXA CORP.			
XX	Galger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordenez N;			
PI	Carter L, Mcneill PD;			
XX	MP1; 2003-598749/56.			
DR	P-PDB; ADD67525.			
XX	New hematological malignancy-related genes and polypeptides, useful for			

	PT	screening anti-cancer agents, and generating antibodies or immunocjugates for treating e.g. multiple myeloma cell or chronic lymphocytic leukemia.
	PS	Claim 1; SEQ ID NO 1; 307pp.; English.
	PX	
	XX	
	CC	The present invention describes an isolated polynucleotide (I), which is overexpressed in haematological malignancies, and which encodes a polypeptide or an immunogenic fragment of the polypeptide. Also described: (1) an isolated polypeptide; (2) an expression vector comprising (i) operably linked to an expression control sequence; (3) a host cell comprising an expression vector; (4) an isolated antibody that specifically binds to the polypeptide or its immunogenic fragment; and (5) immunocjugates comprising the antibody above, or an antibody that specifically binds to a polypeptide, or its immunogenic fragment, encoded by (1). (1) has cytostatic and immunosensitulant activities, and can be used in vaccines and immunotherapy. The immunocjugates are useful in the manufacture of a medicament, particularly as active ingredients in a composition for treating cancer, e.g. multiple myeloma cell, chronic lymphocytic leukaemia, B cell leukemias, or lymphomas in humans, sheep, primates, goats, bovines, equines, porcine, lupines, canines or felines. The polynucleotide (I) or polypeptide can be used for screening anti-cancer agents, and generating antibodies or immunocjugates for treating or preventing the above-mentioned diseases. The polynucleotide, polypeptide or antibody can be used for detecting, diagnosing or prognosticating the haematological malignancies described above. The present sequence is used in the exemplification of the present invention.
SEQ	Sequence	2672 BP; 818 A; 611 C; 620 G; 623 T; 0 U; 0 Other;
Query Match	96.3%; Score	2604.6; DB 10; Length 2672;
Best Local Similarity	99.4%; Pred. No. 0;	
Matches 2658;	Conservative 0;	Mismatches 9; Indels 8; Gaps 4
OY	27	CTTCCAGGAGCAATATGGCTGTTCCTCCCAACATGCCTCACCCTCATCTATATCTTTGG 86
Dd	1	CTTCAGAGACAATATGGCTGTTCCTCCCAACATGCCCTCACCTTCATTAATCTTTGG 60
OY	87	CAGCTCAGAGGTCAGCAGCCTCTTGGAACCGCTGAAAGAAGCTGGTTCCTGGTGGG 146
Dd	61	CAGCTCAGAGGTCAGCAGCCTCTTGGAACCGTGAAGAAGACTGGTTCCTGGTGGG 120
OY	147	GCCGTGACTTTCCCCCTGTAAGTCCAAGATAAAGCAATTGACTTATTTGTCTGACCTTC 206
Dd	121	GCCGTGACTTTCCCCCTGTAAGTCCAAGATAAAGCAATTGACTTATTTGTCTGACCTTC 180
OY	207	AACACAAACCCCTCTTGCACATACAGCABAAGGGGGCACTATCATATGTATACCCAAAT 266
Dd	181	AACACAAACCCCTCTTGCACATACAGCABAAAAGGGGGCACTATCATATGTATACCCAAAT 240
OY	267	GCTAATAGGGAGAGTAGTGACTTCCCAGATGGAGCTTCTCCCTGMAAGCTCAGCAAATG 326
Dd	241	GCTAATAGGGAGAGTAGTGACTTCCCAGATGGAGCTTCTCCCTGMAAGCTCAGCAAATG 300
OY	327	AAGAAGAATGACTCAGGGATCTACTATGTGGGATATACAGCTCATCTCCAGCAGCC 386
Dd	301	AAGAAGAATGACTCAGGGATCTACTATGTGGGATATACAGCTCATCTCCAGCAGCC 360
OY	387	TCCACCCAGAGTAGTGTCTGACATGTCTACAGACACCTGTCAAGAGCCATAAGTACCAATG 446
Dd	361	TCCACCCAGAGTAGTGTCTGACATGTCTACAGACACCTGTCAAGAGCCATAAGTACCAATG 420
OY	447	GCTGTCAGAGCAATTAAGATAGGCACTGTGTGACCAATCTGACATGTGATGGAAAT 506
Dd	421	GCTGTCAGAGCAATTAAGATAGGCACTGTGTGACCAATCTGACATGTGATGGAAAT 480
OY	507	GGGGAAGAGATGTATTATACCTGGAAAGGCTCTGGGGCAAGACGCCAATGAGTCCAT 566
Dd	481	GGGGAAGAGATGTATTATACCTGGAAAGGCTCTGGGGCAAGACGCCAATGAGTCCAT 540
OY	567	AATGGATTCATCTCCCATCTCTTGAGAGATGGGGAAGAAATGATATGACCTTATCTGC 626
Dd	541	AATGGATTCATCTCCCATCTCTTGAGAGATGGGGAAGAAATGATATGACCTTATCTGC 600

QY 627 GTTGCAGGAACCTGTGACAGAAATTCTCAAGCCCATCTTGCCAGGAAGCTCTGT 686
| | | | |
Db 601 GTTGCCAGGAACCTGTGACAGAAATTCTCAAGCCCATCTTGCCAGGAAGCTCTGT 660
| | | | |
QY 687 GAAGGTGCTGTATGACCAAGATTCTCCATAGTGTCTCTGTGTCTCTGTGGTGGCC 746
| | | | |
Db 661 GAAGGTGCTGTATGACCAAGATTCTCCATAGTGTCTCTGTGTCTCTGTGGTGGCC 720
| | | | |
QY 747 CTCCTGCTAGTCTCTTGTACTGGGGCTATTCTTGTGTTTCTGAAGAGAGAGACAA 806
| | | | |
Db 721 CTCCTGCTAGTCTCTTGTACTGGGGCTATTCTTGTGTTTCTGAAGAGAGAGACAA 780
| | | | |
QY 807 GAAAGTACATTGAAGAAAGAAAGAGTGAATTGTGCGAAACTCCCTAACATATGC 866
| | | | |
Db 781 GAAAGTACATTGAAGAAAGAAAGAGTGAATTGTGCGAAACTCCCTAACATATGC 840
| | | | |
QY 867 CCCCATTTCTGAGAGAAACACAGAGTACAGACATCCCTCACCTAATAGAACATCTTA 926
| | | | |
Db 841 CCCCATTTCTGAGAGAAACACAGAGTACAGACATCCCTCACCTAATAGAACATCTTA 900
| | | | |
QY 927 AAGGAAGATCCAGCAATACGTTTACTCCATGTGGAATACCGAAAAAGATGGAAT 986
| | | | |
Db 901 AAGGAAGATCCAGCAATACGTTTACTCCATGTGGAATACCGAAAAAGATGGAAT 960
| | | | |
QY 987 CCCCACTGCTGCTACGATGCCAGACACACAAAGCTATTGGCTATGAGAAATGTATC 1046
| | | | |
Db 961 CCCCACTGCTGCTACGATGCCAGACACACAAAGCTATTGGCTATGAGAAATGTATC 1020
| | | | |
QY 1047 TAGACAGCAGTGCATCCCTTAAGTCTGTCTCAAAAAAACAATTCGCGCCCAAG 1106
| | | | |
Db 1021 TAGACAGCAGTGCATCCCTTAAGTCTGTCTCAAAAAAACAATTCGCGCCCAAG 1080
| | | | |
QY 1107 AAAACATCAGAGAAATTCAGTATTGACTAGAAACATCAAGGAAGAAATGAAGAGTT 1166
| | | | |
Db 1081 AAAACATCAGAGAAATTCAGTATTGACTAGAAACATCAAGGAAGAAATGAAGAGTT 1140
| | | | |
QY 1167 GACTTTTTTCAGATTAATATCTGTAGTCTTCTTAAGATTGAAGTTCGTAAATCC 1226
| | | | |
Db 1141 GACTTTTTTCAGATTAATATCTGTAGTCTTCTTAAGATTGAAGTTCGTAAATCC 1200
| | | | |
QY 1227 ATCCACTGCTGAGAAATTCCTCAAAACCGAAGGTTTAATCATCTTCAATCCCAAAATG 1286
| | | | |
Db 1201 ATCCACTGCTGAGAAATTCCTCAAAACCGAAGGTTTAATCATCTTCAATCCCAAAATG 1260
| | | | |
QY 1287 GATTGGAATGTGAGCAAAACATTAATAAAGTCTTGAAGATTCCTTATAGAAATGTA 1346
| | | | |
Db 1261 GATTGGAATGTGAGCAAAACATTAATAAAGTCTTGAAGATTCCTTATAGAAATGTA 1320
| | | | |
QY 1347 ATGCAAGGTCAACATATTAAATGACAGCCTGTGTATTAATGATGCTCCAGGTCAAGT 1406
| | | | |
Db 1321 ATGCAAGGTCAACATATTAAATGACAGCCTGTGTATTAATGATGCTCCAGGTCAAGT 1380
| | | | |
QY 1407 CTGGAATTTCAATCCACAGGGCTTGTGATGTCAGAGATTATACAAAGTCTTGTAC 1466
| | | | |
Db 1381 CTGGAATTTCAATCCACAGGGCTTGTGATGTCAGAGATTATACAAAGTCTTGTAC 1440
| | | | |
QY 1467 AGGAGGGCAAGAAACCAAAACAGACAGCAAGTCCAGCAGAAAGCAGATGCACCTGACA 1526
| | | | |
Db 1441 AGGAGGGCAAGAAACCAAAACAGACAGCAAGTCCAGCAGAAAGCAGATGCACCTGACA 1500
| | | | |
QY 1527 AAATGATGTATTAAATTTGGCTCTAATAATGTCGACACTATGCTGAGCTTACACT 1586
| | | | |
Db 1501 AAATGATGTATTAAATTTGGCTCTAATAATGTCGACACTATGCTGAGCTTACACT 1560
| | | | |
QY 1587 AATTTGTCAAGCTGTCTGTGCTCTCAAGAAATTTGGCTCAAAATGAATGAATCTTTC 1646
| | | | |
Db 1561 AATTTGTCAAGCTGTCTGTGCTCTCAAGAAATTTGGCTCAAAATGAATGAATCTTTC 1620
| | | | |
QY 1647 ATGAGCAGTTGTAGCAGGCTGACACAGATTCAGAGAGGACAGGTTGATCCACAG 1706
| | | | |
Db 1621 ATGAGCAGTTGTAGCAGGCTGACACAGATTCAGAGAGGACAGGTTGATCCACAG 1680
| | | | |

QY 1707 ACTTGAAGGTCAAGTTCACAAAGATGAAGAAATCAGGTAAGTCAATGTTTGGCAGAT 1766
| | | | |
Db 1681 ACTTGAAGGTCAAGTTCACAAAGATGAAGAAATCAGGTAAGTCAATGTTTGGCAGAT 1740
| | | | |
QY 1767 ACTTATTAATGAGAACACAGAAAGTGTCAATGCCCCAAGGCAAGGACCTCCAGCAGGCTTC 1826
| | | | |
Db 1741 ACTTATTAATGAGAACACAGAAAGTGTCAATGCCCCAAGGCAAGGACCTCCAGCAGGCTTC 1800
| | | | |
QY 1827 ATTTATGCACTTGTCTGCAAAAAGAAAGTCTAGTTTTTAAGGCTGTGCGCAAAACCATC 1886
| | | | |
Db 1801 ATTTATGCACTTGTCTGCAAAAAGAAAGTCTAGTTTTTAAGGCTGTGCGCAAAACCATC 1860
| | | | |
QY 1887 CCAATTAAGAGACCCAGTCTGAAGTCACTGTAATCTAGTATGAGAGACTTGAATGCA 1946
| | | | |
Db 1861 CCAATTAAGAGACCCAGTCTGAAGTCACTGTAATCTAGTATGAGAGACTTGAATGCA 1920
| | | | |
QY 1947 GGCAGTGAACCTGTGGGGGCAAGGGGGCAGTGGTACTGTAAACCTTTAAGATGGT 2006
| | | | |
Db 1921 GGCAGTGAACCTGTGGGGGCAAGGGGGCAGTGGTACTGTGTAAACCTTTAAGATGGT 1980
| | | | |
QY 2007 AATTCAATTCATATGATATTATTAAGAACTTACTATGCGGCCGCGCATGTGGCTCACAC 2066
| | | | |
Db 1981 AATTCAATTCATATGATATTATTAAGAACTTACTATGCGGCCGCGCATGTGGCTCACAC 2037
| | | | |
QY 2067 CTGTAAATCCAGCACTTTGGAGGCAAGTGGGTGGTCAATCTGAGTCAAGAGTTCAA 2126
| | | | |
Db 2038 CTGTAAATCCAGCACTTTGGAGGCAAGTGGGTGGTCAATCTGAGTCAAGAGTTCAA 2097
| | | | |
QY 2127 GACAGACCTGGGCAACATGTGAAACCCCATCTCACTAAAGAT--CAAAATTCCTAG 2184
| | | | |
Db 2098 GACAGACCTGGGCAACATGTGAAACCCCATCTCACTAAAGATCAAAATTTGCTAG 2157
| | | | |
QY 2185 CGTGTGTGTGTCACCTGT-ATCCAGCTACTCGAGAGGCAAGGCAATGAGATGCTTG 2243
| | | | |
Db 2158 CGTGTGTGTGTCACCTGTATTCAGTCACTCGAGAGGCAAGGCAATGAGATGCTTG 2217
| | | | |
QY 2244 AACCTGG--AGGTGAGTTGCAATGAGTGAAGTCACTGCACTCCGCGCTTACGCA 2301
| | | | |
Db 2218 AACCTGGAGGTGAGTGGTTCAGTGAAGTGAAGTGCACCTGCACTCCGCGCTTACGCA 2277
| | | | |
QY 2302 ACGAGAGCAAACTCCATTAACAACAACAACACCTGTGTAGTCACTGTGCA 2361
| | | | |
Db 2278 ACGAGAGCAAACTCCATTAACAACAACAACACCTGTGTAGTCACTGTGCA 2337
| | | | |
QY 2362 CGTAAGATGAACATCCCTTACCAACACAGAGTCAACATCTCTTATACTTAAGTGAATAAC 2421
| | | | |
Db 2338 CGTAAGATGAACATCCCTTACCAACACAGAGTCAACATCTCTTATACTTAAGTGAATAAC 2397
| | | | |
QY 2422 ATGGGAAAAGGGAAAAGGGAAATGGCTGTTTGTATATGTTCCCTGACCGCATATCTTGAAT 2481
| | | | |
Db 2398 ATGGGAAAAGGGAAAAGGGAAATGGCTGTTTGTATATGTTCCCTGACCATATCTTGAAT 2457
| | | | |
QY 2482 GGAGACCTCCCTTACCAATGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2541
| | | | |
Db 2458 GGAGACCTCCCTTACCAATGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2517
| | | | |
QY 2542 CAAGATGGGATTTGAGATTAATCTTCTCAGAAAGCATTGTGAAGAAATTTAGCCAGA 2601
| | | | |
Db 2518 CAAGATGGGATTTGAGATTAATCTTCTCAGAAAGCATTGTGAAGAAATTTAGCCAGA 2577
| | | | |
QY 2602 TCTCTCTCCCTTACGCAAAACCTTATTTGATGAAGAAAGTCTTCTTATCTATTAATPA 2661
| | | | |
Db 2578 TCTCTCTCCCTTACGCAAAACCTTATTTGATGAAGAAAGTCTTCTTATCTATTAATPA 2637
| | | | |
QY 2662 AACAGATATTGTGAGATTCACTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2696
| | | | |
Db 2638 AACAGATATTGTGAGATTCACTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2672
| | | | |
RESULT 4
AAC55223
ID AAC55223 standard; cdna; 2780 BP.
XX

AC AAC55223;
XX 16-JAN-2001 (first entry)
XX Human secreted protein gene 3 SEQ ID NO:44.
DE Human secreted protein gene 3 SEQ ID NO:44.
XX Human; secreted protein; cytosolic; immunostimulant; antiproliferative;
KM cardiant; antiarhythmic; antiviral; antibacterial; antifungal; cancer;
KM antiparasitic; neuroprotective; nootropic; antiinflammatory; anti-HIV;
KM antiangiogenic; antiarteriosclerotic; diagnosis; immune disorder; AIDS;
KM autoimmune disease; haematopoietic cell disorder; blood protein disorder;
KM agammaglobulinemia; hyperproliferative disease; Gaucher's disease;
KM cardiovascular disorder; congenital heart defect; pulmonary atresia;
KM arhythmia; ischaemia; angiogenesis related disorder; Crohn's disease;
KM atherosclerosis; neurological disease; Alzheimer's disease; Huntington's;
KM infectious disease; cat-scratch disease; chromosome 1; ss.
XX Homo sapiens.
XX WO200047602-A1.
XX 17-AUG-2000.
XX 08-FEB-2000; 2000WO-US003062.
XX 10-FEB-1999; 99US-0119468P.
XX (HUMA-) HUMAN GENOME SCT INC.
XX Rosen CA, Ruben SM, Ebner R, Young PE, Ni J, Soppet DR;
PI Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence KA, Komatsu G;
XX WPI; 2000-543578/49.
XX P-PSDB; AAB32404.
XX New human nucleic acid encoding secreted proteins, useful in the
PT treatment, prevention or diagnosis of immune disorders (e.g. autoimmune
PT diseases), blood protein disorders and hyperproliferative diseases (e.g.
PT Gaucher's disease).
XX Claim 1; Page 411-412; 488pp; English.
XX The polynucleotide sequences given in AAC55190 to AAC55235 encode the
CC human secreted proteins given in AAB32371 to AAB32484. Human secreted
CC proteins have activities based on the tissues and cells the genes are
CC expressed in. Examples of activities include: cytosolic; immunostimulant
CC ; antiproliferative; cardiant; antiarhythmic; antiviral; antibacterial;
CC antifungal; antiparasitic; neuroprotective; nootropic; antiinflammatory;
CC antidiabetic; anti-HIV; and antiarteriosclerotic. The polynucleotides
CC and polypeptides, or their agonists and antagonists, can be used for
CC treating, preventing or diagnosing immune disorders (e.g. cancer,
CC autoimmune diseases), disorders of haematopoietic cells, blood protein
CC disorders (e.g. agammaglobulinemia), hyperproliferative diseases (e.g.
CC Gaucher's disease), cardiovascular disorders (e.g. congenital heart
CC defects, pulmonary atresia, arhythmia, ischaemia), angiogenesis related
CC disorders (e.g. Crohn's disease, atherosclerosis), neurological diseases
CC (e.g. Alzheimer's disease, Huntington's chorea), infectious diseases
CC (e.g. AIDS, cat-scratch disease and other bacterial, viral, parasitic or
CC fungal diseases). AAC55181 to AAC55189 and AAB32370 represent sequences
CC used in the exemplification of the present invention
XX
XX Sequence 2780 BP; 819 A; 658 C; 652 G; 651 T; 0 U; 0 Other;
SO
Query Match 80.9%; Score 2186.4; DB 3; Length 2780;
Best Local Similarity 90.7%; Pred. No. 0;
Matches 2530; Conservative 0; Mismatches 136; Indels 122; Gaps 14;
QY 26 ACTTCGAGAGCAATATGCTGCTCCCAACATGCTCAACCTCATATATCCCTTG 85
DB 4 ACGAGCAGAGAGCAATATGCTGCTCCCAACATGCTCAACCTCATATATCCCTTG 63
QY 86 GCAAGTCACAGAGCTCAGAGCTTGAGACCCGTGAAAGAGCTGCTCCGTTGCTGG 145
DB 86 GCAAGTCACAGAGCTCAGAGCTTGAGACCCGTGAAAGAGCTGCTCCGTTGCTGG 145

DB 64 GCAAGTCACAGAGCTCAGAGCTTGAGACCCGTGAAAGAGCTGCTCCGTTGCTGG 123
QY 146 GGCCTGACCTTTCCTCCCTGAGTCCAAAGTGAAGTGAATGCTTATGCTGAGCCTT 205
DB 124 GGCCTGACCTTTCCTCCCTGAGTCCAAAGTGAAGTGAATGCTTATGCTGAGCCTT 183
QY 206 CAACACACACCCCTCTTGTCCATACAGCCAGAGGGGGGACATATAGTGAACCCAAA 265
DB 184 CAACACACACCCCTCTTGTCCATACAGCCAGAGGGGGGACATATAGTGAACCCAAA 243
QY 266 TCGTAATAGGAGAGATAGTACCTTCCAGATGAGGCTACTCCCTGAGCTCAGCAACT 335
DB 244 TCGTAATAGGAGAGATAGTACCTTCCAGATGAGGCTACTCCCTGAGCTCAGCAACT 301
QY 326 GAAGAAGAAATGATCAGAGGATGATGATGATGATGATGATGATGATGATGATGATG 385
DB 302 GAAGAAGAAATGATCAGAGGATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 386 CTCACCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 445
DB 361 CTCACCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 446 GGGTCTGACAGAGCAATAGATGAGCACTGTGTGACCAATCTGATGCTGATGAGAAC 505
DB 421 GGGTCTGACAGAGCAATAGATGAGCACTGTGTGACCAATCTGATGCTGATGAGAAC 480
QY 506 TGGGGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 565
DB 481 TGGGGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 536
QY 566 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 625
DB 537 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 596
QY 626 CGTTGCCAGAGAACCTGTGACAGAGAACTTTCAGACCCCATCTTCCAGAGAGCTTG 685
DB 597 CGTTGCCAGAGAACCTGTGACAGAGAACTTTCAGACCCCATCTTCCAGAGAGCTTG 656
QY 686 TGAAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 735
DB 657 TGAAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 716
QY 736 TGTGAGCCCTCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 795
DB 717 AGCTCTTACAGCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 776
QY 796 GAGAGAGACAG 854
DB 777 CAGGCTGGAG 836
QY 855 -----CTTACATATGCCCCA-----TTCTGAGAGAGAGAGAGAGAGAGAG 895
DB 837 TCTCCCTTCTGTGCTGCTCCACCATCTCTGAAGGTGCTGATGAGACCCAGATTC 896
QY 896 CACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
DB 897 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 956
QY 907 -----ACATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 939
DB 957 ATTTCTTGGTTTCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1016
QY 940 GAAATACGTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 999
DB 1017 GAAATACGTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1075
QY 1000 TCAAGTACAGAGACAG 1059
DB 1076 TCAAGTACAGAGACAG 1135
QY 1060 ACTCCCTTAAGTCTGCTCAAAAAAACAATTTCTGGCCCAAGAGAGAGAGAGAGAG 1119
DB 1136 ACTCCCTTAAGTCTGCTCAAAAAAACAATTTCTGGCCCAAGAGAGAGAGAGAGAG 1195

QY 1120 GAATTCATGATTTGACTAGAAACATCAAGAGAAATGAAGAGCTTGTGCTTTTCCAG 1179
| | | | |
Db 1196 GAATTCATGATTTGACTAGAAACATCAAGAGAAATGAAGAGCTTGTGCTTTTCCAG 1255
| | | | |
QY 1180 GATTAATTTATCTGATGCTTTTGAATTTAAGAGTTCGTAAATTCATCTGCTGAG 1239
| | | | |
Db 1256 GATTAATTTATCTGATGCTTTTGAATTTAAGAGTTCGTAAATTCATCTGCTGAG 1315
| | | | |
QY 1240 AATTCCTCAAAACCGAAGGTTTATCACTTCATCCCAAAAATGGAGTTGAAATGTC 1299
| | | | |
Db 1316 AATTCCTCAAAACCGAAGGTTTATCACTTCATCCCAAAAATGGAGTTGAAATGTC 1375
| | | | |
QY 1300 AGCAAAACATTAATAAAAGTCTTAGAATTTCTTAGAATAATGTAATGCAAGTCA 1359
| | | | |
Db 1376 AGCAAAACATTAATAAAAGTCTTAGAATTTCTTAGAATAATGTAATGCAAGTCA 1435
| | | | |
QY 1360 CATATTAAATGACGCTGTTGTATTAATGATGCTCAAGTCACTGCTGAGTTTCAT 1419
| | | | |
Db 1436 CATATTAAATGACGCTGTTGTATTAATGATGCTCAAGTCACTGCTGAGTTTCAT 1495
| | | | |
QY 1420 CCATCCAGGAGCTTGGATGTCAGGATTTATCCAAAGATCTTGTACAGAGAGGCAAGA 1479
| | | | |
Db 1496 CCATCCAGGAGCTTGGATGTCAGGATTTATCCAAAGATCTTGTACAGAGAGGCAAGA 1555
| | | | |
QY 1480 GACCAAAACAGACAGACAAGTCCAGAGAGAGAGATGCACTTGACAAATAATGATGAT 1539
| | | | |
Db 1556 GACCAAAACAGACAGACAAGTCCAGAGAGAGAGATGCACTTGACAAATAATGATGAT 1615
| | | | |
QY 1540 AATGGCTCTAATAACTATGTGCTCCAGCACTATGCTGAGCTTCACTAATTTGCTGAG 1599
| | | | |
Db 1616 AATGGCTCTAATAACTATGTGCTCCAGCACTATGCTGAGCTTCACTAATTTGCTGAG 1675
| | | | |
QY 1600 TGCTGCTGAGCTCATGAATTTGGCTCCAAATGAATGAATCTTTCATGAGAGTTGTA 1659
| | | | |
Db 1676 TGCTGCTGAGCTCATGAATTTGGCTCCAAATGAATGAATCTTTCATGAGAGTTGTA 1735
| | | | |
QY 1660 GCAGGCTGACACAGATTTCCAGAGAGGCGCAGGTGTGATCCACAGAGCTTGAAGTCAA 1719
| | | | |
Db 1736 GCAGGCTGACACAGATTTCCAGAGAGGCGCAGGTGTGATCCACAGAGCTTGAAGTCAA 1795
| | | | |
QY 1720 AGTTCCAAAGATGAAGATCAGGGTACGTGACCAATGTTGGCAGATCTAATAATGAGA 1779
| | | | |
Db 1796 AGTTCCAAAGATGAAGATCAGGGTACGTGACCAATGTTGGCAGATCTAATAATGAGA 1855
| | | | |
QY 1780 CACAGAAGTGTGATGAGCCCAAGAGACAGGACCTCCAGGCGCTCATTTAATGCACTTG 1839
| | | | |
Db 1856 CACAGAAGTGTGATGAGCCCAAGAGACAGGACCTCCAGGCGCTCATTTAATGCACTTG 1915
| | | | |
QY 1840 TGCTGCAAAAAGAAAGTCTAGGTTTTAAGGCTGTGCAGAACCCATCCCAATTAAGAGAC 1899
| | | | |
Db 1916 TGCTGCAAAAAGAAAGTCTAGGTTTTAAGGCTGTGCAGAACCCATCCCAATTAAGAGAC 1975
| | | | |
QY 1900 CGAGTCTGAAGTCACTTGAATCTAAGTGTAGAGAACTTGGAGTCAAGGAGTGAAGCTG 1959
| | | | |
Db 1976 CGAGTCTGAAGTCACTTGAATCTAAGTGTAGAGAACTTGGAGTCAAGGAGTGAAGCTG 2035
| | | | |
QY 1960 GTGGGCAAGGAGGAGAGTGGTACTGTAAACCTTTAAAGATGTTAATTCATTTCAATA 2019
| | | | |
Db 2036 GTGGGCAAGGAGGAGAGTGGTACTGTAAACCTTTAAAGATGTTAATTCATTTCAATA 2095
| | | | |
QY 2020 GATATTTATTAAGAACCTATATGCGGCCCGGAGTGTGCTCAACCTGTATCCACAG 2079
| | | | |
Db 2096 GATATTTATTAAGAACCTATATGCGGCCCGGAGTGTGCTCAACCTGTATCCACAG 2152
| | | | |
QY 2080 ACTTTGGAGGCGCAAGGTGGGTGGTCAATTTGAGTGCAGAGTTCAAGACCACTGGCC 2139
| | | | |
Db 2153 ACTTTGGAGGCGCAAGGTGGGTGGTCAATTTGAGTGCAGAGTTCAAGACCACTGGCC 2212
| | | | |
QY 2140 AACATGTTGAACCCCATCTCTACTAAAGAT--CAAAATTTGTGAGCGGTGGTGGTGC 2197
| | | | |
Db 2213 AACATGTTGAACCCCATCTCTACTAAAGATCAAAAAATTTGTGAGCGGTGGTGGTGC 2272
| | | | |

QY 2199 ACTGTG-ATCCAGTACTCGAGAGGCCAAGGCATGAGAAATGCTTGAACCTTG--AGGT 2254
| | | | |
Db 2273 ACTGTGAATCCAGCTACTCGAGAGGCCAAGGCATGAGAAATGCTTGAACCTTGAGGTG 2332
| | | | |
QY 2255 GAGGTTGACGTAGAGTGAATGGACCACTGACCTCCGCTTAAGGCAACGAGAGAAAC 2314
| | | | |
Db 2333 GAGGTTGACGTAGAGTGAATGGACCACTGACCTCCGCTTAAGGCAACGAGAGAAAC 2392
| | | | |
QY 2315 TCCAAATCAAAACAAACAAACCAACACCTGTGTAGAGTCAAGTGGCAGCTAAGATGAA 2374
| | | | |
Db 2393 TCCAAATCAAAACAAACAAACCAACACCTGTGTAGAGTCAAGTGGCAGCTAAGATGAA 2452
| | | | |
QY 2375 TCCCTACCAACACAGAGCTCACCATCTCTTAATCTTAAGTGAATAATGGGAAAGGGA 2434
| | | | |
Db 2453 TCCCTACCAACACAGAGCTCACCATCTCTTAATCTTAAGTGAATAATGGGAAAGGGA 2512
| | | | |
QY 2435 AAGGGGAATGGCTGCTTTTGAATATGTTCCCTGACCGCATATCTTGAATGAGACCTCC 2494
| | | | |
Db 2513 AAGGGGAATGGCTGCTTTTGAATATGTTCCCTGACCATATCTTGAATGAGACCTCC 2572
| | | | |
QY 2495 CCAAGTGAATGAAGTGTGAATACTTAATAAATAATGCTTGGGCAAGATGGGATT 2554
| | | | |
Db 2573 CCAAGTGAATGAAGTGTGAATACTTAATAAATAATGCTTGGGCAAGATGGGATT 2632
| | | | |
QY 2555 GAGGATTAATCTTCTGCAAAAAGGCAATTTGGAAGAAATGAGCAATCTCTCCCTAC 2614
| | | | |
Db 2633 GAGGATTAATCTTCTGCAAAAAGGCAATTTGGAAGAAATGAGCAATCTCTCCCTAC 2692
| | | | |
QY 2615 TGCAAAACCTTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 2674
| | | | |
Db 2693 TGCAAAACCTTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 2752
| | | | |
QY 2675 AGATTCACTAATAAAAAAAAAAAAAAAAAA 2702
| | | | |
Db 2753 AGATTCACTAATAAAAAAAAAAAAAAAAAA 2780
| | | | |
RESULT 5
ADQ24216
ID ADQ24216 strand: DNA; 3651 BP.
XX
AC ADQ24216;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7036.
XX
KW soft tissue sarcoma; cytosolic; gene therapy; vaccine; screening; human;
KW ds.
XX
OS Homo sapiens.
XX
PN MO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003MO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnick A;
XX
DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 7036; 210pp; English.
XX

CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC DNA of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.

XX Sequence 3651 BP; 996 A; 837 C; 769 G; 926 T; 0 U; 123 Other;

Query Match 63.9%; Score 1728.8; DB 12; Length 3651;

Best Local Similarity 99.2%; Pred. No. 0; Mismatches 7; Indels 8; Gaps 4;

DB 912 AATAGCAATCCCTAAGAGAGATCCAGCAATACGGTTTACTCAGCTGGAAATACCG 971
 DB 1752 AAGAGCAATCCCTAAGAGAGATCCAGCAATACGGTTTACTCAGCTGGAAATACCG 1811
 QY 972 AAAAAAGATGGAATCCCACTCACTGCTCAGATGCCAGACACCAAGGCTATTGGCC 1031
 DB 1812 AAAAAAGATGGAATCCCACTCACTGCTCAGATGCCAGACACCAAGGCTATTGGCC 1871
 QY 1032 TATGAGAAATGTTATCTAGACAGCAGTGCATCCCTAAGTCTGCTCAAAAAAACA 1091
 DB 1872 TATGAGAAATGTTATCTAGACAGCAGTGCATCCCTAAGTCTGCTCAAAAAAACA 1931
 QY 1092 ATTCTCGGCCCAAGAGAAACAATCAAGAAATTCATGATTTGACTGAAACATCAAGA 1151
 DB 1932 ATTCTCGGCCCAAGAGAAACAATCAAGAAATTCATGATTTGACTGAAACATCAAGA 1991
 QY 1152 AGAATGAAGAAGCTTGAATTTTTCAGAGTAATTAATCTGATGCTTCTTGAATTTA 1211
 DB 1992 AGAATGAAGAAGCTTGAATTTTTCAGAGTAATTAATCTGATGCTTCTTGAATTTA 2051
 QY 1212 AGAGTGTGTAATTCATCAGCTGCTGAGAAATCTCTCAAAACCAAGAGGTTTATCACT 1271
 DB 2052 AGAGTGTGTAATTCATCAGCTGCTGAGAAATCTCTCAAAACCAAGAGGTTTATCACT 2111
 QY 1272 TCATCCCAAAAAATGGGATTTGATGTCAGCAAAACATAAAAAAGTCTTGAAGATT 1331
 DB 2112 TCATCCCAAAAAATGGGATTTGATGTCAGCAAAACATAAAAAAGTCTTGAAGATT 2171
 QY 1332 CCTATAGAAATGTAAATGCAAGTCAACATATTATGACAGGCTGTGTTATTAATGATG 1391
 DB 2172 CCTATAGAAATGTAAATGCAAGTCAACATATTATGACAGGCTGTGTTATTAATGATG 2231
 QY 1392 GCTTCAGAGTCAAGTGTGAGTTTCAATTCATCCAGAGGCTTGGATGTCAGGATTAATAC 1451
 DB 2232 GCTTCAGAGTCAAGTGTGAGTTTCAATTCATCCAGAGGCTTGGATGTCAGGATTAATAC 2291
 QY 1452 AAGAGTCTTGGCTACAGAGAGGCAAGAAACCAAAACAGACAGCAAGTCCAGAGAAC 1511
 DB 2292 AAGAGTCTTGGCTACAGAGAGGCAAGAAACCAAAACAGACAGCAAGTCCAGAGAAC 2351
 QY 1512 AGATGACACTGACAAAAATGGATGTATTATTTGCTCTAATTAATGATGCTCCAGCACTA 1571
 DB 2352 AGATGACACTGACAAAAATGGATGTATTATTTGCTCTAATTAATGATGCTCCAGCACTA 2411
 QY 1572 TGCTGAGCTTAACATTAATGGTTCAGAGCTGCTGTCCCTCATGAATTTGGCTCAAT 1631
 DB 2412 TGCTGAGCTTAACATTAATGGTTCAGAGCTGCTGTCCCTCATGAATTTGGCTCAAT 2471
 QY 1632 GAAAGAACTACTTTCATGAGAGAGTTGAGAGGCTGACCAAGATTTCCAGAGAGGCGAG 1691
 DB 2472 GAAAGAACTACTTTCATGAGAGAGTTGAGAGGCTGACCAAGATTTCCAGAGAGGCGAG 2531
 QY 1692 GTGTGATTCACAGAGACTTGAAGGTCAAAGTTCAAAAGATGAAGATTCAGGGTACCTGA 1751

DB 2532 GTGTGATTCACAGAGACTTGAAGGTCAAAGTTCAAAAGATGAAGATTCAGGGTACCTGA 2591
 QY 1752 CCATGTTTGGCAGATCTATTAATGAGACACAGAAAGTGTGATGCCCCAGAGACAGAGAC 1811
 DB 2592 CCATGTTTGGCAGATCTATTAATGAGACACAGAAAGTGTGATGCCCCAGAGACAGAGAC 2651
 QY 1812 CTCAGCAGAGCTTCATTTATGCACTTGTGTGCAAAAGAAAGTCTAAGTTTAAAGGCT 1871
 DB 2652 CTCAGCAGAGCTTCATTTATGCACTTGTGTGCAAAAGAAAGTCTAAGTTTAAAGGCT 2711
 QY 1872 GTGCCAGAACCCATCCCAATTAAGAGACCGAGTCTGAAGTCAATTTGATTAAGTGA 1931
 DB 2712 GTGCCAGAACCCATCCCAATTAAGAGACCGAGTCTGAAGTCAATTTGATTAAGTGA 2771
 QY 1932 GGAGACTTGGAGTCAAGCAGTGAAGTGTGTGGGACAGGGGGGAGTGGTCACTTGTAA 1991
 DB 2772 GGAGACTTGGAGTCAAGCAGTGAAGTGTGTGGGACAGGGGGGAGTGGTCACTTGTAA 2831
 QY 1992 CCTTAAAGATGGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2051
 DB 2832 CCTTAAAGATGGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2888
 QY 2052 CATGTGGCTCACACCTGTATTCACAGCACTTTGGAGGCAAGTGGTGGTCACTGTG 2111
 DB 2889 CATGTGGCTCACACCTGTATTCACAGCACTTTGGAGGCAAGTGGTGGTCACTGTG 2948
 QY 2112 AGGTCAAGAGTTCAAGACCAAGCTGGCCAAATGTGTAAACCCCATCTCTAATAAGAT 2170
 DB 2949 AGGTCAAGAGTTCAAGACCAAGCTGGCCAAATGTGTAAACCCCATCTCTAATAAGAT 3008
 QY 2171 -CAAAATTTGCTGAGGCTGAGTGGTGGTCACTGTG-ATCCAGAGCTCTGAGAGGCGAAG 2228
 DB 3009 CAAAAATTTGCTGAGGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 3068
 QY 2229 CATGAGAAATGCTTGAACCTGG--AGGTGAGTTTGCAGTGAAGTGAAGTGAAGTGAAG 2286
 DB 3069 CATGAGAAATGCTTGAACCTGGAGGAGTGGAGGTTGAGTGAAGTGAAGTGAAGTGAAG 3128
 QY 2287 ACTCGGCTTGAAGCAAGAGCAAACTCCATATCAACAAACAAACAAACCTGTGC 2346
 DB 3129 ACTCGGCTTGAAGCAAGAGCAAACTCCATATCAACAAACAAACAAACCTGTGC 3188
 QY 2347 TAGGTCACTGGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2406
 DB 3189 TAGGTCACTGGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3248
 QY 2407 ACTTAAGTGAAGAAACATGGGGAAGGGAATGCTGCTTTGATATGTTCCCTG 2466
 DB 3249 ACTTAAGTGAAGAAACATGGGGAAGGGAATGCTGCTTTGATATGTTCCCTG 3308
 QY 2467 ACGCATATCTTGAATGAGACCTCCCTAACAAGTGAAGAAAGTGTGAAGAACTTAATA 2526
 DB 3309 ACGCATATCTTGAATGAGACCTCCCTAACAAGTGAAGAAAGTGTGAAGAACTTAATA 3368
 QY 2527 CAAATGCTTGTGGGCAAGAAATGGAGTTGAGTATCTTCTCGAAGAGGCAATGTGA 2586
 DB 3369 CAAATGCTTGTGGGCAAGAAATGGAGTTGAGTATCTTCTCGAAGAGGCAATGTGA 3428
 QY 2587 AGGAATTTGAGCAGATCTCTCCCTAATGCAAAACCTTATTTAGTAAAGAGTCTTCT 2646
 DB 3429 AGGAATTTGAGCAGATCTCTCCCTAATGCAAAACCTTATTTAGTAAAGAGTCTTCT 3488
 QY 2647 TTAATATCTTAATTAACAGATATTTGTGAGATTCACATTAAGAAAGAAAGAAAGAA 2702
 DB 3489 TTAATATCTTAATTAACAGATATTTGTGAGATTCACATTAAGAAAGAAAGAAAGAA 3544

RESULT 6
 AAX00615
 ID AAX00615 standard; DNA; 1412 BP.
 XX
 AC AAX00615;

XX		
DT	25-MAR-1999	(first entry)
XX		
DE	Human secreted protein gene 5 clone HASAV70.	
XX		
KW	Human; secreted protein; fusion protein; gene therapy; protein therapy;	
KW	diagnosis; tissue cancer; tumour; neurodegenerative disorder; leukaemia;	
KW	developmental abnormality; foetal deficiency; blood allergy; renal; ds;	
KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;	
KW	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;	
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;	
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;	
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.	
OS	Homo sapiens.	
XX		
PN	WO842738-A1.	
XX		
PD	01-OCT-1998.	
XX		
PF	19-MAR-1998; 98MO-US005311.	
XX		
PR	21-MAR-1997; 97US-0041276P.	
PR	21-MAR-1997; 97US-0041277P.	
PR	21-MAR-1997; 97US-0041281P.	
PR	21-MAR-1997; 97US-0042344P.	
PR	30-MAY-1997; 97US-0048069P.	
PR	30-MAY-1997; 97US-0048094P.	
PR	30-MAY-1997; 97US-0048095P.	
PR	30-MAY-1997; 97US-0048096P.	
PR	30-MAY-1997; 97US-0048099P.	
PR	30-MAY-1997; 97US-0048131P.	
PR	30-MAY-1997; 97US-0048135P.	
PR	30-MAY-1997; 97US-0048154P.	
PR	30-MAY-1997; 97US-0048160P.	
PR	30-MAY-1997; 97US-0048186P.	
PR	30-MAY-1997; 97US-0048187P.	
PR	30-MAY-1997; 97US-0048188P.	
PR	30-MAY-1997; 97US-0048351P.	
PR	30-MAY-1997; 97US-0048352P.	
PR	30-MAY-1997; 97US-0048355P.	
PR	30-MAY-1997; 97US-0050937P.	
PR	05-AUG-1997; 97US-0054804P.	
PR	19-AUG-1997; 97US-0056370P.	
PR	02-OCT-1997; 97US-0060862P.	
XX		
PA	(HMDA-) HUMAN GENOME SCI INC.	
XX		
F1	Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Duan R, Hu J;	
P1	Florence KW, Olsen HS, Ebner R, Brewer LA, Moore PA, Shi Y,	
P1	Lafleur DW, Ni J;	
XX		
DR	WPI: 1999-070066/06. P-FSDB; AAM67811.	
PT	New isolated human genes and the secreted polypeptides they encode -	
PT	useful for diagnosis and treatment of e.g. cancers, neurological	
PT	disorders, immune diseases, inflammation or blood disorders.	
XX		
PS	Claim 1; Page 171-172; 385pp; English.	
XX		
CC	This sequence represents a nucleic acid molecule which encodes a secreted	
CC	human protein. The gene number, and the clone it is derived from, are	
CC	detailed in the descriptor line. The gene can be used to generate fusion	
CC	proteins by linking to the gene to a human immunoglobulin Fc portion	
CC	(e.g. AA00602) for increasing the stability of the fused protein as	
CC	compared to the human protein only. The invention relates to 87 novel	
CC	genes and their fragments (nucleic acid sequences: AA00611-X00724; amino	
CC	acid sequences AAM67807-W68004) which are useful for preventing, treating	
CC	or ameliorating medical conditions e.g. by protein or gene therapy. Also,	
CC	pathological conditions can be diagnosed by determining the amount of the	
CC	new polypeptides in a sample or by determining the presence of mutations	
CC	in the new polynucleotides. Specific uses are described for each of the	

CC	87 polynucleotides, based on which tissues they are most highly expressed
CC	In (see AAX00611 For described uses)
XX	
SQ	Sequence 1412 BP; 439 A; 310 C; 310 G; 348 T; 0 U; 5 Other;
	Query Match 50.6%; Score 1369.4; DB 2; Length 1412;
	Best Local Similarity 99.0%; Pred. No. 0;
	Matches 1384; Conservative 2; Mismatches 11; Indels 1; Gaps 1
OY	616 CCTTCATCTGCGTGGCCAGAAACCTGTCAGCAGAACTCTCAAGCCCCATCTTGCCA 675
DB	2 CCTTCATCTGCGTGGCCAGAAACCTGTCAGCAGAACTCTCAAGCCCCATCTTGCCA 61
OY	676 GGAAGCTCTGGGAAGTGTCTGTATGACCAGATTCTCCTCATGTCTCTGTCTCTCC 735
DB	62 GGAAGCTCTGGGAAGTGTCTGTATGACCAGATTCTCCTCATGTCTCTGTCTCTCC 121
OY	736 TGTGGTGCCTCCCTCCGTCACTCTCTTTGTACTGGGGCTATTTCTTTGGTTCTGAAGA 795
DB	122 TGTGGTGCCTCCCTCCGTCACTCTCTTTGTACTGGGGCTATTTCTTTGGTTCTGAAGA 181
OY	796 GAGAGAGACAAGAGAATGACATTGGAAGAGAAGAGAGTGGACATTTGTCCGGAACCTC 855
DB	182 GAGAGAGACAAGAGAATGACATTGGAAGAGAAGAGAGTGGACATTTGTCCGGAACCTC 241
OY	856 CTAACTATTTGCCCATTTCTGGAAGAACACAGAGTAGACACATTCCTCACATAA 915
DB	242 CTAACTATTTGCCCATTTCTGGAAGAACACAGAGTAGACACATTCCTCACATAA 301
OY	916 GAACAACTCTTAAAGGAAGATCCAGAAATACGGTTTACTCCACTGTGAAATACGAAAA 975
DB	302 GAACAACTCTTAAAGGAAGATCCAGAAATACGGTTTACTCCACTGTGAAATACGAAAA 361
OY	976 AGATGGAAAATCCCACCTCACTGCTCAAGATGCCAGACACACAAAGGCTATTGGCTATG 1033
DB	362 AGATGGAAAATCCCACCTCACTGCTCAAGATGCCAGACACACAAAGGCTATTGGCTATG 421
OY	1036 AGAATGTTATCTAGACAGACAGGACCTCCCTTAATCTCTGCTCAAAAAAACAATTC 109
DB	422 AGAATGTTATCTAGACAGACAGGACCTCCCTTAATCTCTGCTCAAAAAAACAATTC 481
OY	1096 TCGGCCCAAGAAAAACAATCAGAAATTCCTGATTGACTAGAAACATCAAGAGAAGA 115
DB	482 TCGGCCCAAGAAAAACAATCAGAAATTCCTGATTGACTAGAAACATCAAGAGAAGA 541
OY	1156 TGAAGAACGTTGACTTTTTTCCAGAGATTAATTCTCTGATCTCTTTAGATTAAAG 121
DB	542 TGAAGAACGTTGACTTTTTTCCAGAGATTAATTCTCTGATCTCTTTAGATTAAAG 601
OY	1216 TTTCGTAATTCATCCACTGCTGAGAAAATCTCCTCAACCCAGAAAGTTTAATCACTCAT 127
DB	602 TTTCATTAATTCATCCACTGCTGAGAAAATCTCCTCAACCCAGAAAGTTTAATCACTCAT 661
OY	1276 CCCAAAAATGGGAATTTGTAATGTCAAGAAACCATTAAAAAAAGTGGCTTAGAAGTATTCCTA 1331
DB	662 CCCAAAAATGGGAATTTGTAATGTCAAGAAACCATTAAAAAAAGTGGCTTAGAAGTATTCCTA 721
OY	1336 TGAAGAAATTAATGCAAGSTCAACACATTTTAATGCAACCTGTGTGATTAATGATGGCTC 139
DB	722 TAAAAAATTAATGCAAGSTCAACACATTTTAATGCAACCTGTGTGATTAATGATGGCTC 781
OY	1396 CAGGTCAGTGTCTGGAGTTTCATTTCATCCACAGGGCTTGGATGTGAGATTATACCAAGA 145
DB	782 CAGGTCAGTGTCTGGAGTTTCATTTCATCCACAGGGCTTGGATGTGAGATTATACCAAGA 841
OY	1456 GTCTTGTCTACAGAGGGCAAAGAACCAAAAACAGACAGACAAAGTCCAGCAGAAAGCAT 151
DB	842 GTCTTGTCTACAGAGGGCAAAGAACCAAAAACAGACAGACAAAGTCCAGCAGAAAGCAT 901
OY	1516 GCACCTGACAAAAATGATGTATTATTTATTTGGCTCTTAATACATTTGGCCACAGACATATGCT 157
DB	902 GCACCTGACAAAAATGATGTATTATTTATTTGGCTCTTAATACATTTGGCCACAGACATATGCT 961

Oy	1576	GAGCTTACACTAAATTTGGTCACAGCGTGTCTGCGCTTCATGAAAATTGGCTCAATGAAAT	1635
Db	962	GAGCTTACACTAAATTTGGTCACAGCATCTGTCTGGCTTCATGAAAATTGGCTCAATGAAAT	1021
Oy	1636	GAACTACTTTGATGAGCAGTTGTAGACAGGCCCTGACACACAGATTTCCACAGAGGCCAGGTGT	1693
Db	1022	GAACTACTTTGATGAGCAGTTGTAGACAGGCCCTGACACACAGATTTCCACAGAGGCCAGGTGT	1081
Oy	1696	GGATTCACACAGACCTTTGAAGGTTCAAAGTTCACAAAGATGAAGATCAAGGTTAGCTGACCAT	1755
Db	1082	GGATTCACACAGACCTTTGAAGGTTCAAAGTTCACAAAGATGAAGATCAAGGTTAGCTGACCAT	1141
Oy	1756	GTTTTGSCAGATACTATAATGAGAGACACAGAAGTGTGCATGTGGCCCAAGAGACAGACCTCC	1815
Db	1142	GTTTTGSCAGATACTATAATGAGAGACACAGAAGTGTGCATGTGGCCCAAGAGACAGACCTCC	1201
Oy	1816	AGCCAGGCTTCATTTATGACCACTGTGTCTGCAAAAAGAAAAGTCTAGAGTTTAAAGCTGTGC	1875
Db	1202	AGCCAGGCTTCATTTATGACCACTGTGTCTGCAAAAAGAAAAGTCTAGAGTTTAAAGCTGTGC	1260
Oy	1876	CAGAACCCATCCCAATTAAGAGACCGAGCTGGAAGTCACTTGAATCTGTGTGTAAGAG	1935
Db	1261	CAGAACCCATCCCAATTAAGAGACCGAGCTGGAAGTCACTTGAATCTGTGTGTAAGAG	1320
Oy	1936	ACTTGGAGTCAGGACAGTGAAGCTGGTGGGACACGGGGGACAGTGGGTACTTGTAAACCTT	1995
Db	1321	ACTTGGAGTCAGGACAGTGAAGCTGGTGGGACACGGGGGACAGTGGGTANTGTAAACCTTT	1380
Oy	1996	TAAAGATGTGTTAATTCAT 2013	
Db	1381	TAAAGATGTGTTAATTCAT 1398	

RESULT 7	ACCS5224	standard; cDNA, 1412 BP.
XX	ACCS5224	
XX	ACCS5224	
DT	16-JUN-2001	(first entry)
DE	Human secreted protein gene 3 SEQ ID NO:45.	
XX		
KW	Human; secreted protein; cytosolic; immunostimulant; antiproliferative; cardiant; antiarhythmic; antiviral; antibacterial; antifungal; cancer; antiapoptotic; neuroprotective; nocotropic; antiinflammatory; anti-HIV; antiangiogenic; antiatherosclerotic; diagnosis; immune disorder; AIDS; autoimmune disease; haemotopoietic cell disorder; blood protein disorder; agammaglobulinaemia; hyperproliferative disease; Gaucher's disease; cardiovascular disorder; congenital heart defect; pulmonary atresia; arrhythmia; ischaemia; angiogenesis related disorder; Crohn's disease; atherosclerosis; neurological disease; Alzheimer's disease; Huntington's infectious disease; cat-scratch disease; chromosome 1; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200047602-A1.	
XX		
PD	17-AUG-2000.	
XX		
PF	08-FEB-2000; 2000MO-US003062.	
XX		
PR	10-FEB-1999; 99US-0119468P.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Ruben SM, Ebner R, Young PE, Ni J, Soppet DR; Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence KA, Komatsoulis G; WPI: 2000-543578/49.	
XX		
DR	P-PSDB; AAB32405.	
XX		
PT	New human nucleic acids encoding secreted proteins, useful in the	

PT	treatment, prevention or diagnosis of immune disorders (e.g. autoimmune diseases), blood protein disorders and hyperproliferative diseases (e.g. Gaucher's disease).
PS	Claim 1; Page 413; 488bp; English.
XX	
CC	The polynucleotide sequences given in AAC55190 to AAC55235 encode the human secreted proteins given in AAB32371 to AAB32484. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: cytostatic; immunostimulant; antiproliferative; cardiant; anticholinergic; antiviral; antibacterial; antifungal; antiparasitic; neuroprotective; nootropic; antiinflammatory; antiangiogenic; anti-HIV; and antiarteriosclerotic. The polynucleotides and polypeptides, or their agonists and antagonists, can be used for treating, preventing or diagnosing immune disorders (e.g. cancer, autoimmune diseases), disorders of haematopoietic cells, blood protein disorders (e.g. agammaglobulinemia), hyperproliferative diseases (e.g. Gaucher's disease), cardiovascular disorders (e.g. congenital heart defects, pulmonary atresia, arrhythmias, ischemia), angiogenesis related disorders (e.g. Croun's disease, atherosclerosis), neurological diseases (e.g. Alzheimer's disease, Huntington's chorea), infectious diseases (e.g. AIDS, cat-scratch disease and other bacterial, viral, parasitic or fungal diseases). AAC55181 to AAC55189 and AAB32370 represent sequences used in the exemplification of the present invention
CC	
XX	
SQ	Sequence 1412 BP; 439 A; 310 C; 310 G; 348 T; 0 U; 5 Other;
Query Match	50.6%; Score 1369.4; DB 3; Length 1412;
Best Local Similarity	99.0%; Pred. No. 0;
Matches 1384; Conservative	2; Mismatches 11; Indels 1; Gaps 14;
Oy	616 CTTTCATCTGCGTTGCCAGAACCCCTGTGACAGAAACTTCTCAAGCCCATCTCTGCCA 675
Db	2 CCTTCATCTGCGTTGCCAGAACCCCTGTGACAGAAACTTCTCAAGCCCATCTCTGCCA 61
Oy	676 GGAAGCCTCTGGAAGTGCCTGCTATGACCCAGATTCTCATAGTCTCCTGCTGCTCC 735
Db	62 GGAAGCCTCTGGAAGTGCCTGCTATGACCCAGATTCTCATAGTCTCCTGCTGCTCC 121
Oy	736 TGTGGTGACCCTCCTGCTCAGTCTCTTTTGACGTGGGCTATTTCTTTGGTTTCTGAAGA 795
Db	122 TGTGGTGACCCTCCTGCTCAGTCTCTTTTGACGTGGGCTATTTCTTTGGTTTCTGAAGA 181
Oy	796 GAGAGAGACAAAGAGATGACATTGAAGAGAAAGAGAGAGATGGACATTTGTGGGAAATCTC 855
Db	182 GAGAGAGACAAAGAGATGACATTGAAGAGAAAGAGAGATGGACATTTGTGGGAAATCTC 241
Oy	856 CTTAACATATGCCCCCATTTCTGSAAGAACACAGAGTACGACACAATCCTTCACTAATA 915
Db	242 CTTAACATATGCCCCCATTTCTGSAAGAACACAGAGTACGACACAATCCTTCACTAATA 301
Oy	916 GAAACAATCCTTAAGAAAGATCCAGACAAATAGGTTTACTCCAGTGGGAAATACCGAANA 975
Db	302 GAAACAATCCTTAAGAAAGATCCAGACAAATAGGTTTACTCCAGTGGGAAATACCGAANA 361
Oy	976 AGATGGAAGAAATCCCCACTCACTGCTCAAGATCCAGACACACCAAGGCTATTTGCTATG 1035
Db	362 AGATGGAAGAAATCCCCACTCACTGCTCAAGATCCAGACACACCAAGGCTATTTGCTATG 421
Oy	1036 AGAATGTTATCTAGACAGAGTGCATCTCCCTAAGTCTGTGCTCAAAAAAAAAACAATTC 1095
Db	422 AGAATGTTATCTAGACAGAGTGCATCTCCCTAAGTCTGTGCTCAAAAAAAAAACAATTC 481
Oy	1096 TCGGCCCAAGAAAGAAACAATCGAAGAAATTCACTGATTTGACTAGAAACATCAAGAGAAAGA 1155
Db	482 TCGGCCCAAGAAAGAAACAATCGAAGAAATTCACTGATTTGACTAGAAACATCAAGAGAAAGA 541
Oy	1156 TGAAGAAAGTTGACTTTTTCAGAGATAAATATCTCTGATGCTCTTTAGATTAAAGAG 1215
Db	542 TGAAGAAAGTTGACTTTTTCAGAGATAAATATCTCTGATGCTCTTTAGATTAAAGAG 601
Oy	1216 TTGCTAATTCATCACTGCTGAGAAATCTCTCAAAACCAAGAGTTTATCATCTTTCAT 1275
Db	TTGCTAATTCATCACTGCTGAGAAATCTCTCAAAACCAAGAGTTTATCATCTTTCAT 1275

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Db      602 TTCATATTCATCACTGCTGAGAAATCTCTCTCAAAACCCAGAGGTTTAATCATCTTCAT 661
QY      1276 CCCAAATAATGGAGTTGTGAATGTGACAGAAACCATATAAAAAAGGCTTAGAAGATTCTTA 1335
Db      662 CCCAAATAATGGAGTTGTGAATGTGACAGAAACCATATAAAAAAGGCTTAGAAGATTCTTA 721
QY      1336 TGAATAATGTAATGCAAGGTCAACATATTATGACAGGCTGTGTATTAATGATGAGCTC 1395
Db      722 TAAAAATGTAATGCAAGGTCAACATATTATGACAGGCTGTGTATTAATGATGAGCTC 781
QY      1396 CAGGTAGTGTCTGAGGTTTCATTCATCCAGGGGTTTGGATGTCAAGATTAATCAACAA 1455
Db      782 CAGGTAGTGTCTGAGGTTTCATTCATCCAGGGGTTTGGATGTCAAGATTAATCAACAA 841
QY      1456 GTCTTGCTACAGAGAGGCAAGAACCAAAAACAGACAGACAAAGTCCAGACAGAGAGAT 1515
Db      842 GTCTTGCTACAGAGAGGCAAGAACCAAAAACAGACAGACAAAGTCCAGACAGAGAGAT 901
QY      1516 GCACCTGACAAAAATGATGATTAATTTGAGCTCTATTAATCTATGTGCCAGACATATGCT 1575
Db      902 GCACCTGACAAAAATGATGATTAATTTGAGCTCTATTAATCTATGTGCCAGACATATGCT 961
QY      1576 GAGCTTACACTAATTTGTGACAGAGTGTCTGTGCTCTCATGAAATTTGGCTCCAAATGAAT 1635
Db      962 GAGCTTACACTAATTTGTGACAGAGTGTCTGTGCTCTCATGAAATTTGGCTCCAAATGAAT 1021
QY      1636 GAACCTACTTTCATGAGCAGTTGTGAGCAGGCTTGACCAAGATTCCAGAGGGCCAGGTGT 1695
Db      1022 GAACCTACTTTCATGAGCAGTTGTGAGCAGGCTTGACCAAGATTCCAGAGGGCCAGGTGT 1081
QY      1696 GGATCCACAGAGACTTGAAGGTCAAAGTTCACAAAAGATGAAGATCAGGGTACGTGACAT 1755
Db      1082 GGATCCACAGAGACTTGAAGGTCAAAGTTCACAAAAGATGAAGATCAGGGTACGTGACAT 1141
QY      1756 GTTTGGCAATCTATTAATGAGACACAGAAAGTCAATGAGGCCCAAGACAGACACTTC 1815
Db      1142 GTTTGGCAATCTATTAATGAGACACAGAAAGTCAATGAGGCCCAAGACAGACACTTC 1201
QY      1816 ASCCAGGCTTCAATTTATGCACTGTGCTGCATAAAAGAAAGTCTAGGTTTAAAGGCTGTGC 1875
Db      1202 ASCCAGGCTTCAATTTATGCACTGTGCTGCATAAAAGAAAGTCTAGGTTTAAAGGCTGTGC 1260
QY      1876 CAGAACCCATCCCAATTAAGAGACCGAGTCTGAAAGTCACTTTGAATCTTAATGAGAG 1935
Db      1261 CAGAACCCATCCCAATTAAGAGACCGAGTCTGAAAGTCACTTTGAATCTTAATGAGAG 1320
QY      1936 ACTTGAGTCAAGCAGTGAAGTGTGAGGCAACGGGGGGCAGTGGTAACTTTAACTTT 1995
Db      1321 ACTTGAGTCAAGCAGTGAAGTGTGAGGCAACGGGGGGCAGTGGTAACTTTAACTTT 1380
QY      1996 TAAAGATGGTTAATTCAT 2013
Db      1381 TAAAGATGGTTAATTCAT 1398

RESULT 8
ADA40261
ID      ADA40261 standard; cDNA; 1412 BP.
XX
AC      ADA40261;
XX
DT      20-NOV-2003 (first entry)
XX
DE      Human secreted protein encoding cDNA.
XX
KW      Human; secreted protein; cancer; hyperproliferative disorder;
KW      rheumatoid arthritis; autoimmune disorder; hematopoietic disorder;
KW      anaemia; allergic reaction; asthma; cardiovascular disorder;
KW      wound healing; cytotoxic; immunosuppressive; nootropic; neuroprotective;
KW      antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW      vulnerrary; cardiant; gene therapy; 88.
XX
OS      Homo sapiens.
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XX      XX
PN      WO2002102993-A2.
XX      27-DEC-2002.
PD      19-MAR-2002; 2002WO-US008123.
XX      21-MAR-2001; 2001US-0277340P.
PR      19-JUL-2001; 2001US-0306171P.
PR      13-NOV-2001; 2001US-0331287P.
XX      (HUMA-) HUMAN GENOME SCT INC.
XX      Rosen CA, Ruben SM;
PI      WPI; 2003-175238/17.
DR      New human secreted proteins and nucleic acid molecules, useful for
PT      preparing a diagnostic or pharmaceutical composition for diagnosing,
PT      preventing or treating cancer or other hyperproliferative disorder,
PT      asthma, allergies or AIDS.
XX      Claim 9; SEQ ID NO 643; 3205bp; English.
PS      The invention relates to novel genes ADA39629-ADA40565 and proteins
XX      ADA40566-ADA41501 for human secreted proteins, useful for preventing,
XX      treating or ameliorating medical conditions e.g. by protein or gene
XX      therapy. The polypeptides, nucleic acid molecules, antibodies or their
XX      fragments, and agonists or antagonists that bind to the polypeptide are
XX      useful for preparing a diagnostic or pharmaceutical composition for
XX      diagnosing or treating cancer or other hyperproliferative disorder. The
XX      polypeptides and nucleic acid molecules are also useful for detecting,
XX      preventing, diagnosing, prognosticating, treating or ameliorating cancer
XX      or other hyperproliferative disorders including neoplasms, autoimmune
XX      disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
XX      erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
XX      anaemia), haematopoietic or haematological disorders (e.g. anaemia,
XX      thrombocytopenia), allergic reactions including asthma or eczema,
XX      inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
XX      bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
XX      Alzheimer's disease or Parkinson's disease), cardiovascular disorders
XX      (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
XX      fungal or viral infections including HIV/AIDS), or wound healing and
XX      disorders of epithelial cell proliferation. The nucleic acids are also
XX      useful for chromosome identification, radiation hybrid mapping or long-
XX      range restriction mapping, as molecular weight markers, or as
XX      hybridization or diagnostic probes. The polypeptides and antibodies are
XX      useful for providing immunological probes for differential identification
XX      of the tissues immunohistochemistry assays. Note: The sequence data for
XX      CC this patent did not form part of the printed specification, but was
XX      CC obtained in electronic format directly from WIPO at
XX      CC ftp.wipo.int/pub/published_pct_sequences.
SQ      Sequence 1412 BP; 439 A; 310 C; 310 G; 348 T; 0 U; 5 Other;

Query Match      50.6%; Score 1369.4; DB 8; Length 1412;
Best Local Similarity 99.0%; Pred. NO. 0;
Matches 1384; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY      616 CCTTATCTGCTGCTGCCAGAGAACTCTGTGAGCAAGAACTTCTGAAGCCCATCTTGCCA 675
Db      2 CCTTATCTGCTGCTGCCAGAGAACTCTGTGAGCAAGAACTTCTGAAGCCCATCTTGCCA 61
QY      676 GGAAGCTCTGGAAGAGTGTGTAATGACCAAGATTCCTCCATGTGCTCCGTGCTCC 735
Db      62 GGAAGCTCTGTAAGAGTGTGTAATGACCAAGATTCCTCCATGTGCTCCGTGCTCC 121
QY      736 TGTGTGCTCCCTCTGCTGAGTCTCTTGTGTAAGTGGGCTAATTTCTTTGGTTTGAAGA 795
Db      122 TGTGTGCTCCCTCTGCTGAGTCTCTTGTGTAAGTGGGCTAATTTCTTTGGTTTGAAGA 181
QY      796 GAGAGAGCAAGAGAGTATTCATTTGAAGAGAGAGAGTGAACATTTGTGGGAAACTC 855
Db      181 GAGAGAGCAAGAGAGTATTCATTTGAAGAGAGAGAGTGAACATTTGTGGGAAACTC 855
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Db 182 GAGAGAGACAAGAGTAGTACATTGAGAGAAAGAGTGGACATTTGTGGAAATC 241
 Qy 856 CTAAATATGCCCCCATTTTGGAGAGAACACAGATACACACAAATCCCTCACCTAAT 915
 Db 242 CTAAATATGCCCCCATTTTGGAGAGAACACAGATACACACAAATCCCTCACCTAAT 301
 Qy 916 GAAACAATCTTAAAGAGATCCAGCAATACGGTTTCTCCACTGTGGAAATACCGAAA 975
 Db 302 GAACATCTTAAAGAGATCCAGCAATACGGTTTCTCCACTGTGGAAATACCGAAA 361
 Qy 976 AGATGAAAAATCCCACTCACTGCTCAGATGCCAGACACAAAGGCTATTTGGCTATG 1035
 Db 362 AGATGAAAAATCCCACTCACTGCTCAGATGCCAGACACAAAGGCTATTTGGCTATG 421
 Qy 1036 AGAATGTTATCTAGACAGCATGCACTCCCTAAGTCTGTCTCAAAAAAACAATTC 1095
 Db 422 AGAATGTTATCTAGACAGCATGCACTCCCTAAGTCTGTCTCAAAAAAACAATTC 481
 Qy 1096 TCGGCCCCAAGAAAAACATCAGAAATTCAGTATTTAGTAAACATCAAGAGAA 1155
 Db 482 TCGGCCCCAAGAAAAACATCAGAAATTCAGTATTTAGTAAACATCAAGAGAA 541
 Qy 1156 TGAAGAACGTTGACTTTTTCAGAGATAAATATCTGTAGTCTCTTAAATTAAG 1215
 Db 542 TGAAGAACGTTGACTTTTTCAGAGATAAATATCTGTAGTCTCTTAAATTAAG 601
 Qy 1216 TTGTAATTTCTATCTCACTGCTGAGAAATCTCTCAAAACCAAGAGTTTAACTTCAT 1275
 Db 602 TTATATTTCTATCTCACTGCTGAGAAATCTCTCAAAACCAAGAGTTTAACTTCAT 661
 Qy 1276 CCCAAAAATGGGAATTTGAAATGTGAGCAAAACCATAAAAAAGCTTAAAGATTCCTA 1335
 Db 662 CCCAAAAATGGGAATTTGAAATGTGAGCAAAACCATAAAAAAGCTTAAAGATTCCTA 721
 Qy 1336 TAGAAATGTAATGCAAGTCAACATATTAATGACAGCTGTGTAATTAATGAGCTC 1395
 Db 722 TAAAAATGTAATGCAAGTCAACATATTAATGACAGCTGTGTAATTAATGAGCTC 781
 Qy 1396 CAGGTCAAGTCTGAGATTTTCAATCCAGGGCTTGGATGTGAGATTAATCCAGA 1455
 Db 782 CAGGTCAAGTCTGAGATTTTCAATCCAGGGCTTGGATGTGAGATTAATCCAGA 841
 Qy 1456 GTCTGTACAGAGGGGCAAGAAAGACAAACAGACAGCAAGTCCAGCAGAAAGCAT 1515
 Db 842 GTCTGTACAGAGGGGCAAGAAAGACAAACAGACAGCAAGTCCAGCAGAAAGCAT 901
 Qy 1516 GCACTGACAAAAATGATGTAATTAATGCTATTAATGATGCTGAGCACTATGCT 1575
 Db 902 GCACTGACAAAAATGATGTAATTAATGCTATTAATGATGCTGAGCACTATGCT 961
 Qy 1576 GAGCTTACACTAATTTGTCAGACGCTGCTGCTCATGAAATTTGGCTCCAAATGAT 1635
 Db 962 GAGCTTACACTAATTTGTCAGACGCTGCTGCTCATGAAATTTGGCTCCAAATGAT 1021
 Qy 1636 GAACTACTTTTCAGAGAGTTTGAAGGCTGAGCCAGATTCCTCCAGAGGGCCAGGTG 1695
 Db 1022 GAACTACTTTTCAGAGAGTTTGAAGGCTGAGCCAGATTCCTCCAGAGGGCCAGGTG 1081
 Qy 1696 GATTCACAGAGACTTGAAGGTCAAAAGTTCAAAAGATGAAGAAATCAGGATAGTCAAT 1755
 Db 1082 GATTCACAGAGACTTGAAGGTCAAAAGTTCAAAAGATGAAGAAATCAGGATAGTCAAT 1141
 Qy 1756 GTTTGGCAGATTAATTAATGAGACACAGAAAGTGTGATGGCCCAAGACAGAGACTCC 1815
 Db 1142 GTTTGGCAGATTAATTAATGAGACACAGAAAGTGTGATGGCCCAAGACAGAGACTCC 1201
 Qy 1816 AGCAGGCTTCAATTATGACCTGTGCTGCAAAAAGAAAGCTAGGTTTAAAGGCTGTC 1875
 Db 1202 AGCAGGCTTCAATTATGACCTGTGCTGCAAAAAGAAAGCTAGGTTTAAAGGCTGTC 1260
 Qy 1876 CAGAACCCATCCCAATTAAGAGACCGAGTCTGAAGTCAATTTGTAATCTAGTGTAGAG 1935
 Db 1261 CAGAACCCATCCCAATTAAGAGACCGAGTCTGAAGTCAATTTGTAATCTAGTGTAGAG 1320

Qy 1936 ACTTGGATGACGAGTGAAGTCTGTGGGGCACGGGGGGCAGTGGTACTTGTAAACCTT 1995
 Db 1321 ACTTGGATGACGAGTGAAGTCTGTGGGGCACGGGGGGCAGTGGTACTTGTAAACCTT 1380
 Qy 1996 TAAAGATGTTAATTCAT 2013
 Db 1381 TAAAGATGTTAATTCAT 1398
 RESULT 9
 ADA56425
 ID ADA56425 standard; DNA: 1412 BP.
 XX
 AC ADA56425:
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Gene encoding human secreted protein #32.
 XX
 KM immunosuppressive; antiinflammatory; antisthmatic; antiallergic;
 KM cyclostatic; cerebroprotective; neuroprotective; nootropic;
 KM cardiovascular; antiarteriosclerotic; gene therapy;
 KM human secreted protein; immune disorder; inflammation;
 KM respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
 KM inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
 KM multiple sclerosis; ischemic brain injury; Parkinson's disease;
 KM Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
 KM triple helix formation; antisense gene therapy; forensic biology; de;
 KM gene.
 XX
 OS Homo sapiens.
 XX
 PN W02002102994-A2.
 XX
 PD 27-DEC-2002.
 XX
 PF 19-MAR-2002; 2002MO-US008278.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 PI Rosen CA, Ruben SM;
 PI
 DR WPI; 2003-167512/16.
 DR P-PSDB; ADA57321.
 DR
 XX
 XX
 PT New human secreted polypeptides and polynucleotides, useful for
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
 PT conditions, respiratory disorders, cancers, CNS disorders, or
 PT neurodegenerative disorders.
 XX
 PS Claim 21, SEQ ID NO 614; 1754bp; English.
 PS
 XX
 XX
 CC The invention relates to 592 new human secreted polypeptides useful for
 CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
 CC conditions, respiratory disorders, cancers, CNS disorders, or
 CC neurodegenerative disorders, or polypeptides comprising an amino acid
 CC sequence at least 95% identical to the new sequences. The polypeptides,
 CC antibodies or antibody fragments that bind to the polypeptides, nucleic
 CC acids encoding the polypeptides, agonists or antagonists that binds to
 CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
 CC compositions for diagnosing, treating or preventing an e.g. immune
 CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
 CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
 CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
 CC (e.g. multiple sclerosis or ischemic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
 CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
 CC polynucleotides are useful for chromosome identification, chromosome

CC mapping, for controlling gene expression through triple helix formation
 CC or antisense DNA or RNA, in gene therapy, for identifying individuals
 CC from minute biological samples, in forensic biology, and as hybridization
 CC probes. The polypeptides are useful for as molecular weight markers on
 CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
 CC gels, to raise antibodies, for testing biological activities, and for
 CC creating or preventing neural disorders, immune system disorders,
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal, proliferative and/or cancerous diseases. This sequence corresponds
 CC to a gene encoding one of the polypeptide of the invention. Note: The
 CC sequence data for this patent did form part of the printed specification,
 CC but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 1412 BP; 439 A; 310 C; 310 G; 348 T; 0 U; 5 Other;

Query Match 50.6%; Score 1369.4; DB 10; Length 1412;

Best Local Similarity 99.0%; Pred. No. 0;

Matches 1384; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 616 CCTTCATCTGCGTGGCAGGAACCTGTGACAGAAACTTCTCAAGCCCATCTTGCCA 675
 Db 2 CCTCATCTGCGTGGCAGGAACCTGTGACAGAAACTTCTCAAGCCCATCTTGCCA 61
 QY 676 GGAAGCTCTGTGAAGGTGCTGATGACCCAGATTCTTCATGTCCTCTGTCTCC 735
 Db 62 GGAAGCTCTGTGAAGGTGCTGATGACCCAGATTCTTCATGTCCTCTGTCTCC 121
 QY 736 TGTGTGTGCGCCCTGCTCAGTCTTGTACTGGGGCTATTCTTGGTTTCTGAAGA 795
 Db 122 TGTGTGTGCGCCCTGCTCAGTCTTGTACTGGGGCTATTCTTGGTTTCTGAAGA 181
 QY 796 GAGAGAGACAAGAGATGATGAGAGAGAGAGAGAGATGACATTTGTGGGAACTC 855
 Db 182 GAGAGAGACAAGAGATGATGAGAGAGAGAGAGAGATGACATTTGTGGGAACTC 241
 QY 856 CTAACTATATGCCCCCTTCTGAGAGACAAGAGATGACATTTGTGGGAACTC 915
 Db 242 CTAACTATATGCCCCCTTCTGAGAGACAAGAGATGACATTTGTGGGAACTC 301
 QY 916 GAACATCTCTAAAGAGAGATGACAGAAATGAGTTACTCCATGTGGGAAATCCGAAA 975
 Db 302 GAACATCTCTAAAGAGAGATGACAGAAATGAGTTACTCCATGTGGGAAATCCGAAA 361
 QY 976 AGATGAAAATCCCACTGCTCAGATGACAGATGACAGATGACAGATGACAGATG 1035
 Db 362 AGATGAAAATCCCACTGCTCAGATGACAGATGACAGATGACAGATGACAGATG 421
 QY 1036 AGATGTTATCTGACAGAGATGACATCCCTTAAGTCTGTCTCAAAAAAACAATTC 1095
 Db 422 AGATGTTATCTGACAGAGATGACATCCCTTAAGTCTGTCTCAAAAAAACAATTC 481
 QY 1096 TGGGCCCAAGAAACAATCAGAGAAATCAGATTTAAGTGAAGAAACAAGAA 1155
 Db 482 TGGGCCCAAGAAACAATCAGAGAAATCAGATTTAAGTGAAGAAACAAGAA 541
 QY 1156 TGAAGACGTTGACCTTTTCCAGATTAATTAATCTCTGATGCTTCTTTAAGAG 1215
 Db 542 TGAAGACGTTGACCTTTTCCAGATTAATTAATCTCTGATGCTTCTTTAAGAG 601
 QY 1216 TTGCTATTTCCATCCATGCTGAGAAATCTCTCAAAACCAAGGTTTAATCACTTCA 1275
 Db 602 TTGCTATTTCCATCCATGCTGAGAAATCTCTCAAAACCAAGGTTTAATCACTTCA 661
 QY 1276 CCCAAAATGGAATGCTGAATGACAGAAACCAATAAAGGCTTAAGATTCCTTA 1335
 Db 662 CCCAAAATGGAATGCTGAATGACAGAAACCAATAAAGGCTTAAGATTCCTTA 721
 QY 1336 TAGAAATGTAATGCAAGGTGACACATTAATTAAGACGCTGTGTATTAATGATGCTC 1395
 Db 722 TAGAAATGTAATGCAAGGTGACACATTAATTAAGACGCTGTGTATTAATGATGCTC 781
 QY 1396 CAGGTGAGTGTCTGAGTTCAATTCATCCACAGGCTTGAGATGTCAGATTAACCAAGA 1455

Db 782 CAGGTGAGTGTCTGAGTTCAATTCATCCACAGGCTTGAGATGAGATTAATCAAGA 841
 QY 1456 GCTTGATACAGAGAGGCAAGAAAGCAAGAAACAGACAGACATGTCAGAGACAGAT 1515
 Db 842 GCTTGATACAGAGAGGCAAGAAAGCAAGAAACAGACAGACATGTCAGAGACAGAT 901
 QY 1516 GCACCTGACAAATAATGATGATTAATTAATGCTCTTAATAATGATGCTCCAGCATATGCT 1575
 Db 902 GCACCTGACAAATAATGATGATTAATTAATGCTCTTAATAATGATGCTCCAGCATATGCT 961
 QY 1576 GAGCTTAACATTAATGTCAGACGTCGTCTGCTCCCTCATGAATTTGGCTCCAAATGAT 1635
 Db 962 GAGCTTAACATTAATGTCAGACGTCGTCTGCTCCCTCATGAATTTGGCTCCAAATGAT 1021
 QY 1636 GAATCTATTTATGAGACGTTGTATGACAGGCTGACACAGATTTCCAGAGGCGCAGTGT 1695
 Db 1022 GAATCTATTTATGAGACGTTGTATGACAGGCTGACACAGATTTCCAGAGGCGCAGTGT 1081
 QY 1696 GGATCCACAGACATTTGAAGGTCAAAGTTCAAAAGATGAAGATCAGGATGATGACAT 1755
 Db 1082 GGATCCACAGACATTTGAAGGTCAAAGTTCAAAAGATGAAGATCAGGATGATGACAT 1141
 QY 1756 GTTTGGCAGATCTTAATGAGAGACAGAAAGTGTGATGCTCCAAAGACAGACCTCC 1815
 Db 1142 GTTTGGCAGATCTTAATGAGAGACAGAAAGTGTGATGCTCCAAAGACAGACCTCC 1201
 QY 1816 AGCCAGGCTCATTTATGACATGTCGTCGCAAAAGATGATGATTTTAAGGCTGTGC 1875
 Db 1202 AGCCAGGCTCATTTATGACATGTCGTCGCAAAAGATGATGATTTTAAGGCTGTGC 1260
 QY 1876 CAGAACCCATCCCAATAAGAGACCAAGTCTGAAGTCAATTTGAATCTAGTGAAG 1935
 Db 1261 CAGAACCCATCCCAATAAGAGACCAAGTCTGAAGTCAATTTGAATCTAGTGAAG 1320
 QY 1936 ACTTGAGTCAGGCACTGATGAGTGTGGGCAACGGGGGCACTGGGTACTTGAACCTT 1995
 Db 1321 ACTTGAGTCAGGCACTGATGAGTGTGGGCAACGGGGGCACTGGGTACTTGAACCTT 1380
 QY 1996 TAAAGATGTTTAATTCAT 2013
 Db 1381 TAAAGATGTTTAATTCAT 1398

RESULT 10
 AA251572
 ID AA251572 strand: cDNA; 1272 BP.
 XX
 AC AA251572;
 XX
 DT 21-JUN-2000 (first entry)
 XX
 DE Human cell surface immunomodulator-1 (CSIM-1) encoding cDNA.
 XX
 KW Cell surface immunomodulator-1; CSIM-1; cell proliferation; CD84;
 KW differentiation; signal transduction; drug screening; prevention;
 KW treatment; cancer; leukemia; melanoma; immune disorder; AIDS;
 KW rheumatoid arthritis; asthma; atherosclerosis; diabetes mellitus;
 KW emphysema; irritable bowel syndrome; multiple sclerosis; diagnosis;
 KW osteoporosis; psoriasis; microbial infections; cytotoxic; antirheumatic;
 KW antidiabetic; immunosuppressive; antituberculosis; anti-HIV;
 KW antiproliferative; antineoplastic; neuroprotective; osteopathic;
 KW antiproliferative; antimicrobial; human; ss.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FH CDS 38..1045
 FT /*tag= a
 FT /*product= "Cell surface immunomodulator-1"
 FT sig_peptide 38..103
 FT /*tag= b
 FT mat_peptide 104..1042

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FT      /*tag= c
FT      /product= "Mature cell surface immunomodulator-1"
FT      542..574
FT      /*tag= d
FT      /bound_moiety= "Hybridisation probe"

XX      MO200011150-A1.
XX      02-MAR-2000.
XX      24-AUG-1999; 99MO-US019386.
XX      25-AUG-1998; 98US-00155261.
XX      (INCY-) INCYTE PHARM INC.
XX      Lal P, Corley NC, Gorgone GA, Guegler KJ, Patterson C, Baughn MR,
XX      WPI; 2000-246561/21.
XX      P-PSDB; AAY70431.
XX      New human cell surface immunomodulatory polypeptides and polynucleotides
XX      useful for diagnosis, prevention and treatment of cancer and immune
XX      disorders.
XX      Claim 9; Page 63; 70pp; English.
XX      The present sequence is a cDNA identified in Incyte clone 14448, derived
XX      from human promonocyte cell line (THP-1) cDNA library (THP1PLB01). It
XX      encodes human cell surface immunomodulator-1 (CSIMM-1), which is a
XX      regulator of cell proliferation, differentiation, cell-cell communication
XX      and signal transduction. It shows homology to cell surface antigen, CD84.
XX      CSIMM can be used for drug screening, prevention and treatment of cancers
XX      such as leukemia and melanoma, immune disorders such as AIDS, rheumatoid
XX      arthritis, asthma, atherosclerosis, diabetes mellitus, emphysema,
XX      irritable bowel syndrome, multiple sclerosis, osteoporosis, psoriasis and
XX      microbial infections. CSIMM polynucleotide may be used for diagnosis of
XX      CSIMM-associated diseases and as source of probes useful in mapping
XX      naturally occurring genomic sequences
XX      Sequence 1272 BP; 362 A; 322 C; 285 G; 302 T; 0 U; 1 Other;
XX      Query Match 46.5%; Score 1256.6; DB 3; Length 1272;
XX      Best Local Similarity 99.2%; Pred. No. 0;
XX      Matches 1262; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      5 GTGGCTTCATTTGAGTGGTGAAGTTCAGAGAGCAATATGAGTGGTTCCTCCCAACATGCT 64
DB      1 GTGGCTTCATTTGAGTGGTGAAGTTCAGAGAGCAATATGAGTGGTTCCTCCCAACATGCT 60
QY      65 CACCTTCATCTATATCTTTGGCAGCTCAAGGGTCAAGGCTCTGAGCCCGTGAAGA 124
DB      61 CACCTTCATCTATATCTTTGGCAGCTCAAGGGTCAAGGCTCTGAGCCCGTGAAGA 120
QY      125 GCTGTCGCTTCGCTGGTGGGGGCGGTGACTTCCCGCTGAAGCCAAAGTAAAGCAAGT 164
DB      121 GCTGTCGCTTCGCTGGTGGGGGCGGTGACTTCCCGCTGAAGCCAAAGTAAAGCAAGT 180
QY      185 TGACTCATTTGTGAGACTTCAACACACACCCCTCTGTGACCATACAGCCAGAGGGGG 244
DB      181 TGACTCATTTGTGAGACTTCAACACACACCCCTCTGTGACCATACAGCCAGAGGGGG 240
QY      245 CACTATCATATGAGCCCAAAATCGTAATAGGAGAGAGTGAAGTCTCCAGATGAGGCTA 304
DB      241 CACTATCATATGAGCCCAAAATCGTAATAGGAGAGAGTGAAGTCTCCAGATGAGGCTA 300
QY      305 CTCCTGAAGCTCGAGAACTGAAGAAAGATGACTCGGGGATCTACTATATGGGGATATA 364
DB      301 CTCCTGAAGCTCGAGAACTGAAGAAAGATGACTCGGGGATCTACTATATGGGGATATA 360
QY      365 CAGCTCATCACTCCAGAGGCTCCACCCAGAGATAGTGTGATGCTTACAGACACT 424
DB      361 CAGCTCATCACTCCAGAGGCTCCACCCAGAGATAGTGTGATGCTTACAGACACT 420

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QY      425 GTCAAGCCCTAAAGTCACCATGGGTCTGAGAGCAATTAAGAAATGSCACCTGTGTACCAA 484
DB      421 GTCAAGCCCTAAAGTCACCATGGGTCTGAGAGCAATTAAGAAATGSCACCTGTGTACCAA 480
QY      485 TCTGACATGTGTGATGAAATATGGGAAAGAGATGTGATTTATATCTGGAAGCCCTGGG 544
DB      481 TCTGACATGTGTGATGAAATATGGGAAAGAGATGTGATTTATATCTGGAAGCCCTGGG 540
QY      545 GCAGAGACCAATGATGATCCCATATATGGGTTCATCTCTCCCATCTCTGAGATGGGAGA 604
DB      541 GCAGAGACCAATGATGATCCCATATATGGGTTCATCTCTCCCATCTCTGAGATGGGAGA 600
QY      605 AAGTATATGACCTTATCATGCTGGGTGCAAGAAACCTGTGAGAGAACTTCTCAAGCC 664
DB      601 AAGTATATGACCTTATCATGCTGGGTGCAAGAAACCTGTGAGAGAACTTCTCAAGCC 660
QY      665 CATCTTGGCCAGAGACCTGTGAGAGATGTGATGATCCAGATTCCTCATGGTCTT 724
DB      661 CATCTTGGCCAGAGACCTGTGAGAGATGTGATGATCCAGATTCCTCATGGTCTT 720
QY      725 CTTGTGCTCTCTGTGGTGGTCCCTCTGCTCACTCTTTGTACTGGGGTATTTCTTTG 784
DB      721 CTTGTGCTCTCTGTGGTGGTCCCTCTGCTCACTCTTTGTACTGGGGTATTTCTTTG 780
QY      785 GTTTCGAAAGAGAGAGACAAAGAGATCAATTGAAGAAAGAGAGTGAACATTTG 844
DB      781 GTTTCGAAAGAGAGAGACAAAGAGATCAATTGAAGAAAGAGAGTGAACATTTG 840
QY      845 TCGGAAACCTCTAATATATGCCCCATCTGAGAGAAACACAGATGACACAAATCCC 904
DB      841 TCGGAAACCTCTAATATATGCCCCATCTGAGAGAAACACAGATGACACAAATCCC 900
QY      905 TCACACTAATAGAAATCTTAAGAGATCCAGAAATACGGTTTACTCTGACTGTGA 964
DB      901 TCACACTAATAGAAATCTTAAGAGATCCAGAAATACGGTTTACTCTGACTGTGA 960
QY      965 AATACGAAAAAATGAAAAATCCCACTCACTGCTCAGATGCGCAGACACCAAGGCT 1024
DB      961 AATACGAAAAAATGAAAAATCCCACTCACTGCTCAGATGCGCAGACACCAAGGCT 1020
QY      1025 ATTGGCTATGAGAAATGTTATCTAGACAGAGTGCATCCCTTAAGTCTGTCTCAAAA 1084
DB      1021 ATTGGCTATGAGAAATGTTATCTAGACAGAGTGCATCCCTTAAGTCTGTCTCAAAA 1080
QY      1085 AAAAACAATTCGCCCCAAGAAACAAATCAGAAATTCATGATTTGACTAGAAACA 1144
DB      1081 AAAAACAATTCGCCCCAAGAAACAAATCAGAAATTCATGATTTGACTAGAAACA 1140
QY      1145 TCAAGAGAAATGAAAGATGATCTTTTCCAGAGATTAATATCTGATGCTCTTT 1204
DB      1141 TCAAGAGAAATGAAAGATGATCTTTTCCAGAGATTAATATCTGATGCTCTTT 1200
QY      1205 AGATTTAAGAGTTCGTAATTTCCATCTGACTGTGAGAAATCTCTCAAAACCAAGATTT 1264
DB      1201 AGATTTAAGAGTTCGTAATTTCCATCTGACTGTGAGAAATCTCTCAAAACCAAGATTT 1260
QY      1265 AATCACTTCATC 1276
DB      1261 AATCACTTCATC 1272

RESULT 11
ACCT2129
ID ACC72129 standard; DNA; 1082 BP.
XX
AC ACC72129;
XX
DT 07-JUL-2003 (first entry)
XX
DE Human NOV27a coding sequence.
XX
KM Human; NOV; antidiabetic; anorectic; antibacterial; virucide;

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RESULT 12
AAZ65040
ID AAZ65040 standard; cDNA; 1076 BP.
XX
AC AAZ65040;
XX
DT 05-Apr-2000 (first entry)
XX
DE Membrane-bound protein PRO118 encoding cDNA.
XX
KM Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIR ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX
OS Homo sapiens.
XX
PN WC0963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99MO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.
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 PR 16-SEP-1998; 98US-0106534P.
 PR 12-JAN-1999; 99US-0115565P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PI Wood WJ, Yuan J;
 XX
 DR WPI; 2000-072883/06.
 DR P-PSDB; AAY66701.
 XX
 PT Membrane-bound proteins and related nucleotide sequences.
 PS Claim 2; Fig 170; 822pp; English.
 XX
 CC The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIE
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
 CC also be useful for the preparation of PRO polypeptides, especially by
 CC recombinant techniques
 CC
 SQ Sequence 1076 BP; 291 A; 285 C; 255 G; 245 T; 0 U; 0 Other;
 QY Query Match 39.8%; Score 1076; DB 3; Length 1076;
 DB Best Local Similarity 100.0%; Pred. No. 3.8e-273;
 Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GTGGCTTCATTTCAGTGGCTGACTTCCAGAGAGCAATATGCTGTTCCTCCCAATGCTT 64
 DB 1 GTGGCTTCATTTCAGTGGCTGACTTCCAGAGAGCAATATGCTGTTCCTCCCAATGCTT 60
 QY 65 CACCCATCATATATATCTTTGGCAGCTCAAGGGTCAGAGAGCTCTGAGACCGGTGAAGA 124
 DB 61 CACCCATCATATATATCTTTGGCAGCTCAAGGGTCAGAGAGCTCTGAGACCGGTGAAGA 120
 QY 125 GCTGTGCGGTCGTTGTGTGGGCGCTGACTTTCCTCCCTGAGTCCAAAGTAAGCACT 184
 DB 121 GCTGTGCGGTCGTTGTGTGGGCGCTGACTTTCCTCCCTGAGTCCAAAGTAAGCACT 180
 QY 185 TGACTTATTTGTGTGAGACTTCAACAAACCTCTTGTGCACATACAGCCGAGAGGGG 244
 DB 181 TGACTTATTTGTGTGAGACTTCAACAAACCTCTTGTGCACATACAGCCGAGAGGGG 240
 QY 245 CACTATCATATGAGACCAAAATGCTAATGGGAGAGATGACTTCCCGAGATGAGAGCTA 304
 DB 241 CACTATCATATGAGACCAAAATGCTAATGGGAGAGATGACTTCCCGAGATGAGAGCTA 300
 QY 305 CTCCTGAGAGCTCAGCAAACTGAGAAGATGACTCAGGAGATCTATATGTGGGATATA 364
 DB 301 CTCCTGAGAGCTCAGCAAACTGAGAAGATGACTCAGGAGATCTATATGTGGGATATA 360
 QY 365 CAGCTCATCATCTCAGAGAGCTTCAACCAAGAGATGCTGTGATGTCTTACGAGAGACT 424

DB 361 CAGCTCATCATCTCCAGAGAGCCCTCCACCAGAGATGACTGTGATGTCTTACAGACACT 420
 QY 425 GTCAAGAGCTTAAGTACACATGAGTCTGAGAGCAATAGATGAGACCTGTGTACCA 484
 DB 421 GTCAAGAGCTTAAGTACACATGAGTCTGAGAGCAATAGATGAGACCTGTGTACCA 480
 QY 485 TCTGACATGCTGCATGGAACATGAGGAAAGAGATGATTTATACCTGAAAGCCCTGGG 544
 DB 481 TCTGACATGCTGCATGGAACATGAGGAAAGAGATGATTTATACCTGAAAGCCCTGGG 540
 QY 545 GCAGAGAGCAATGAGTCCCATATATGGGTCCATCTCTCCCACTCTCTGAGATGGGAGA 604
 DB 541 GCAGAGAGCAATGAGTCCCATATATGGGTCCATCTCTCCCACTCTCTGAGATGGGAGA 600
 QY 605 AAGTATATGACTTCTGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 664
 DB 601 AAGTATATGACTTCTGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 QY 665 CATCTTGGCAGAGAGCTCTGTGAAGGTGCTGATGACCCAGATTCTCTCATGCTCT 724
 DB 661 CATCTTGGCAGAGAGCTCTGTGAAGGTGCTGATGACCCAGATTCTCTCATGCTCT 720
 QY 725 CTTGTGTCTCTCTGTTGGTGGCCCTCTCTGCTGATCTCTTTGTATGGGGCTATTCTTTG 784
 DB 721 CTTGTGTCTCTCTGTTGGTGGCCCTCTCTGCTGATCTCTTTGTATGGGGCTATTCTTTG 780
 QY 785 GTTTCGAGAGAGAGAGAGAGAGAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAG 844
 DB 781 GTTTCGAGAGAGAGAGAGAGAGAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAG 840
 QY 845 TCGGAGAACTCTTAACATATGCCCCCATTTCTGAGAGAGAGAGAGAGAGAGAGAGAG 904
 DB 841 TCGGAGAACTCTTAACATATGCCCCCATTTCTGAGAGAGAGAGAGAGAGAGAGAGAG 900
 QY 905 TACACTAATATGAACAATCTTAAGAGAGATCCACCAATATAGCTTACTCACTGTGGA 964
 DB 901 TACACTAATATGAACAATCTTAAGAGAGATCCACCAATATAGCTTACTCACTGTGGA 960
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 DB 961 AATACCGAAGAAAGATGAGAAATCCCACTCACTGCTCAGATGCGAGACACCAAGGCT 1020
 QY 1025 ATTTCCTATGAGAGATGTTATCTATAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 DB 1021 ATTTCCTATGAGAGATGTTATCTATAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1076
 RESULT 13
 AAS46020
 ID AAS46020 strand; cDNA; 1076 BP.
 XX
 AC AAS46020;
 XX
 DT 18-DEC-2001 (first entry)
 DE Human DNA encoding PRO polypeptide sequence #96.
 XX
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; sheep; ss;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
 KW PCR primer.
 XX
 OS Homo sapiens.
 XX
 PN WO200168848-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US006520.
 XX
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.

PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 26-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
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PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
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PR 11-APR-2000; 2000US-0196820P.
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PR 18-APR-2000; 2000US-0198121P.
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PR 25-APR-2000; 2000US-0199397P.
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PR 03-MAY-2000; 2000US-0201516P.
PR 13-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Deenoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI: 2001-602746/68.
DR P-PSDB; AAU29119.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
PS Claim 2; Fig 191; 774pp; English.
XX
CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
SQ Sequence 1076 BP; 291 A; 285 C; 255 G; 245 T; 0 U; 0 Other;

Query Match 39.8%; Score 1076; DB 4; Length 1076;
Best Local Similarity 100.0%; Pred. No. 3.8e-273;

Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GTGGCTTCAATTAGTGGCTGACTTCCAGAGACCAATATGCGTTCCTCCCAATGAGCCT 64
DB 1 GTGGCTTCAATTAGTGGCTGACTTCCAGAGACCAATATGCGTTCCTCCCAATGAGCCT 60
QY 65 CACCTCATCTATATCTTTTGGAGCTCAACAGGTCAGACCTCTGACCCCTGAAAGA 124
DB 61 CACCTCATCTATATCTTTTGGAGCTCAACAGGTCAGACCTCTGACCCCTGAAAGA 120
QY 125 GCTGTGCGTTCCGTTGTGGGGCCGTGACTTTCCCTGAGTCCAAAGTAAGCAAGT 184
DB 121 GCTGTGCGTTCCGTTGTGGGGCCGTGACTTTCCCTGAGTCCAAAGTAAGCAAGT 180
QY 185 TGACTCTATTGTCTGGAACCTTGAAACAACCCCTCTTGTCACATACAGCAGAGGGG 244
DB 181 TGACTCTATTGTCTGGAACCTTGAAACAACCCCTCTTGTCACATACAGCAGAGGGG 240
QY 245 CACTATCATATGATGACCAAAATGCTAATAGGAGAGATGACTTCCAGATGAGGCTA 304
DB 241 CACTATCATATGATGACCAAAATGCTAATAGGAGAGATGACTTCCAGATGAGGCTA 300
QY 305 CTCCCTGAAGCTCAGAAACTGAAAGAATGACTCAGGATCTATATGTGGGATATA 364
DB 301 CTCCCTGAAGCTCAGAAACTGAAAGAATGACTCAGGATCTATATGTGGGATATA 360
QY 365 CAGCTCATCTCCACAGCCCTCCACCCAGAGTACGTCTGCAATGTCTACAGACACT 424
DB 361 CAGCTCATCTCCACAGCCCTCCACCCAGAGTACGTCTGCAATGTCTACAGACACT 420
QY 425 GTCAAGCCTTAAGTCAACCATGAGTCTGCAAGACCAATTAAGATGACCTGTGACAA 484
DB 421 GTCAAGCCTTAAGTCAACCATGAGTCTGCAAGACCAATTAAGATGACCTGTGACAA 480
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DB 601 AAGTATATGACCTTATCATCTGCTTCCAGAACTCTGACAGAACTTCTCAAGCC 660
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DB 661 CATCTTGCAGAGAACCTCTGTAAGTGTCTGTGATGACCCAGATTCCTCATGTGCT 720
QY 725 CCTGTCTCTCTGTGTGTGCTCCTCTGTCAGTCTTTTATCTGTGGGCTATTTTCT 784
DB 721 CCTGTCTCTCTGTGTGTGCTCCTCTGTCAGTCTTTTATCTGTGGGCTATTTTCT 780
QY 785 GTTTCGAAGAGAGAGACAAGAAAGTATGAAGAAAGAAAGAGAGTGGACATTTG 844
DB 781 GTTTCGAAGAGAGAGACAAGAAAGTATGAAGAAAGAAAGAGTGGACATTTG 840
QY 845 TCGGGAACCTCTTAATATGCCCCCATTTCTGAGAGAAACACAGATGACACAAATCCC 904
DB 841 TCGGGAACCTCTTAATATGCCCCCATTTCTGAGAGAAACACAGATGACACAAATCCC 900
QY 905 TCACTATATTAACAATCTTAAGAGAGATCCAGAAATAGGTTTACTCTCATGTGGA 964
DB 901 TCACTATATTAACAATCTTAAGAGAGATCCAGAAATAGGTTTACTCTCATGTGGA 960
QY 965 AATACCGAAAAAGATGAAATATCCCATCTGCTCAGATGCCAGACACCAAGGCT 1024
DB 961 AATACCGAAAAAGATGAAATATCCCATCTGCTCAGATGCCAGACACCAAGGCT 1020
QY 1025 ATTGCTTATGAGATGTTATCTTACACAGCAGTGCATCTCCCTAAGTCTTGCTCA 1080
DB 1021 ATTGCTTATGAGATGTTATCTTACACAGCAGTGCATCTCCCTAAGTCTTGCTCA 1076

RESULT 14

AA92080 standard; cDNA; 1076 BP.

AA92080;

15-MAY-2001 (first entry)

Human PRO138 cDNA.

Human; PRO protein; mapping; ss.

Homo sapiens.

MO200116318-A2.

08-MAR-2001.

24-AUG-2000; 2000MO-US023328.

01-SEP-1999; 99MO-US020111.

07-DEC-1999; 99US-0169495P.

09-DEC-1999; 99US-0170262P.

11-JAN-2000; 2000US-0175481P.

18-FEB-2000; 2000MO-US004342.

22-FEB-2000; 2000MO-US004414.

01-MAR-2000; 2000MO-US005601.

03-MAR-2000; 2000US-0187202P.

21-MAR-2000; 2000US-0191007P.

30-MAR-2000; 2000MO-US008439.

25-APR-2000; 2000US-0199397P.

22-MAY-2000; 2000MO-US014042.

05-JUN-2000; 2000US-0209832P.

(GETH) GENENTECH INC.

Baton DL, Flyvareff E, Gerritsen ME, Goddard A, Godowski PJ; Grimaldi CJ, Gurney AL, Katanabe CK, Wood WI;

WPI; 2001-183260/18.

P-PSDB; AAB87548.

Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.

Claim 2; Fig 45; 278bp; English.

The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping

Sequence 1076 BP; 291 A; 285 C; 255 G; 245 T; 0 U; 0 Other;

Query Match 39.8%; Score 1076; DB 4; Length 1076; Best Local Similarity 100.0%; Pred.No.3.8e-273;

Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 GTGGCTTCAATTCAGTGGCTGACCTTCAGAGACCAATATGCTGTTCCCAACATGCTT 64

1 GTGGCTTCAATTCAGTGGCTGACCTTCAGAGACCAATATGCTGTTCCCAACATGCTT 60

65 CACCTCATCTATATCTTTGGCAGCTCAAGGAGTCAAGGCTCTGACCCGTGAAGA 124

61 CACCTCATCTATATCTTTGGCAGCTCAAGGAGTCAAGGCTCTGACCCGTGAAGA 120

125 GCTGGTCCGTTCCGTTGGTGGGCGGTGACTTTCCCGTGAAGTCCAAAGTAAACAAGT 184

121 GCTGGTCCGTTCCGTTGGTGGGCGGTGACTTTCCCGTGAAGTCCAAAGTAAACAAGT 180

185 TGACTCTATTGCTTGGACCTTCCACAACAACCCCTCTTGTCAACATACAGCCGAAGGGGG 244

181 TGACTCTATTGCTTGGACCTTCCACAACAACCCCTCTTGTCAACATACAGCCGAAGGGGG 240

245 CACTATCATATGACCCCAAAATCGTAATAGGAGAGATGACCTTCCAGATGAGGCTTA 304

241 CACTATCATATGACCCCAAAATCGTAATAGGAGAGATGACCTTCCAGATGAGGCTTA 300

305 CTCCTGAAGCTCAGCAAACTGAAGAAGATGACTCAGGATCTACTATGTGGGATATA 364

301 CTCCTGAAGCTCAGCAAACTGAAGAAGATGACTCAGGATCTACTATGTGGGATATA 360

365 CAGCTCATCATCTCCAGAGCCCTCCAGAGAGTACGTGCTGATGCTACAGACACT 424

361 CAGCTCATCATCTCCAGAGCCCTCCAGAGAGTACGTGCTGATGCTACAGACACT 420

425 GTCAAAAGCTTAAAGTCCATATGCTGTCAGAGCAATAGCACTGCTGTACCA 484

421 GTCAAAAGCTTAAAGTCCATATGCTGTCAGAGCAATAGCACTGCTGTACCA 480

485 TCTGACATGCTGATGAAACATGGGAAAGAGATGATTTATACCTGGAAGCCCTGGG 544

481 TCTGACATGCTGATGAAACATGGGAAAGAGATGATTTATACCTGGAAGCCCTGGG 540

545 GCAAGCAGCAATGAGTCCCATATATGAGTCCATCTCTGAGATGGGAGAG 604

541 GCAAGCAGCAATGAGTCCCATATATGAGTCCATCTCTGAGATGGGAGAG 600

605 AAGTATATGACCTTCACTGCTGTTGGTCCAGGAACCTCTGACAGAACTTTCAGGCC 664

601 AAGTATATGACCTTCACTGCTGTTGGTCCAGGAACCTCTGACAGAACTTTCAGGCC 660

665 CATCTTCGAGGAAGCTCTGTAAGTGTGCTGATGACCAAGATCTCCATGATGCT 724

661 CATCTTCGAGGAAGCTCTGTAAGTGTGCTGATGACCAAGATCTCCATGATGCT 720

725 CCTGTGTCTCTGTGTGTGTCGCCCTCTGCTGATGCTCTTGTGATGCTGAGGCTATTTCTTTG 784

721 CCTGTGTCTCTGTGTGTGTCGCCCTCTGCTGATGCTCTTGTGATGCTGAGGCTATTTCTTTG 780

785 GTTTCGAGAGAGAGAGAGAGAGAGATGATGATGAGAGAGAGAGAGAGATGATG 844

781 GTTTCGAGAGAGAGAGAGAGAGAGATGATGATGAGAGAGAGAGAGAGATGATG 840

845 TCGGGAACCTCTCATATATGCCCCCATCTTGGAGAGACAGAGTACGACCAATCCC 904

841 TCGGGAACCTCTCATATATGCCCCCATCTTGGAGAGAGAGAGTACGACCAATCCC 900

905 TCACATATATAGAACATCTTAAAGAGATTCAGCAAAATACGTTTACTCCTGCTGGA 964

901 TCACATATATAGAACATCTTAAAGAGATTCAGCAAAATACGTTTACTCCTGCTGGA 960

965 AATACCGAAAAAGATGAAAAATCCCACTCACTGTCAGATGCCAGACACCAAGGCT 1024

961 AATACCGAAAAAGATGAAAAATCCCACTCACTGTCAGATGCCAGACACCAAGGCT 1020

1025 ATTGCTATGAGATGATATCTATAGACAGAGTGCATCCCTATAGTCTGCTGCTCA 1080

1021 ATTGCTATGAGATGATATCTATAGACAGAGTGCATCCCTATAGTCTGCTGCTCA 1076

RESULT 15

AA94186 standard; cDNA; 1076 BP.

AA94186;

XX 02-APR-2001 (first entry)
DT
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DE Human PRO1138 (UNQ576) nucleotide sequence SEQ ID NO:252.
KW Human; secreted and transmembrane protein; PRO; cytosolic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
KM diagnostic assay; ss.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145638P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
XX (GETH) GENENTECH INC.
XX
PI Aahkenazi AJ, Baker KP, Borstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gertsen ME, Goddard A, Godowski PJ;
PI Gimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
XX WPI; 2001-032160/04.
DR P-PSDB; AAB65224.
XX
XX PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
XX Claim 2; Fig 170; 935p; English.
XX
XX The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF4470 to
CC AAF4470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention

XX
SQ Sequence 1076 BP; 291 A; 285 C; 255 G; 245 T; 0 U; 0 Other;
Query Match 39.8%; Score 1076; DB 5; Length 1076;
Best Local Similarity 100.0%; Pred. No. 3.8e-273;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GTGGCTTCAATTCAGAGGCTGACTTCCAGAGCAATATAGGCTGTTCCCAACATGCTT 64
DB 1 GTGGCTTCAATTCAGAGGCTGACTTCCAGAGCAATATAGGCTGTTCCCAACATGCTT 60
QY 65 CACCTCATCTATATATCTTTGGCAGCTCAAGGCTCAGACGCTTGAAGCAAGCA 124
DB 61 CACCTCATCTATATATCTTTGGCAGCTCAAGGCTCAGACGCTTGAAGCAAGCA 120
QY 125 GCTGTGCGGTTCCGTTGGTGGGCGCTGACTTTCCTCCCTGAAGTCCAAAGTAAAGCAAGT 184
DB 121 GCTGTGCGGTTCCGTTGGTGGGCGCTGACTTTCCTCCCTGAAGTCCAAAGTAAAGCAAGT 180
QY 185 TGACTCATATGCTGAGACCTTCAACCAACCCCTTGTCAACATACAGCCAGAGGGG 244
DB 181 TGACTCATATGCTGAGACCTTCAACCAACCCCTTGTCAACATACAGCCAGAGGGG 240
QY 245 CACTATCATATGAGACCCCAAAATGTAATAGGAGAGATGACTTCCAGATGAGAGCTTA 304
DB 241 CACTATCATATGAGACCCCAAAATGTAATAGGAGAGATGACTTCCAGATGAGAGCTTA 300
QY 305 CTCCTCGAAGCTCAGCAAACTGAAGAAATGACTCAGGATTAATGTGGGATATTA 364
DB 301 CTCCTCGAAGCTCAGCAAACTGAAGAAATGACTCAGGATTAATGTGGGATATTA 360
QY 365 CAGCTCATATCTCAGAGGCTTCCACAGAGATAGGCTGATGATGAGAGACCTT 424
DB 361 CAGCTCATATCTCAGAGGCTTCCACAGAGATAGGCTGATGATGAGAGACCTT 420
QY 425 GTCAAGACCTTAAGTCAATGAGGCTGAGAGCAATGAATGAGCACTGTGTGACAA 484
DB 421 GTCAAGACCTTAAGTCAATGAGGCTGAGAGCAATGAATGAGCACTGTGTGACAA 480
QY 485 TCTGACATGCTGATGAGAACTGAGGAGAGATGATTTATCTGAGAGGCTTGG 544
DB 481 TCTGACATGCTGATGAGAACTGAGGAGAGATGATTTATCTGAGAGGCTTGG 540
QY 545 GCAAGAGCAATGAGTCCATTAATGGGTCCATCCCTCCATCTCTGAGATGGGAG 604
DB 541 GCAAGAGCAATGAGTCCATTAATGGGTCCATCCCTCCATCTCTGAGATGGGAG 600
QY 605 AAGTATATGAGACCTTATCTGCGTTGCCAGAACTGTGAGAGAACTTCTCAAGCC 664
DB 601 AAGTATATGAGACCTTATCTGCGTTGCCAGAACTGTGAGAGAACTTCTCAAGCC 660
QY 665 CATCTTCCAGAGAACCTTGTGAAGTGTGCTGTGATGACCCAGATTCCTCATGTGCTT 724
DB 661 CATCTTCCAGAGAACCTTGTGAAGTGTGCTGTGATGACCCAGATTCCTCATGTGCTT 720
QY 725 CCTGTGCTTCTGTGTGGTGGCTTCTCTGCTCACTCTTTGATGAGGCTATTTCTTTG 784
DB 721 CCTGTGCTTCTGTGTGGTGGCTTCTCTGCTCACTCTTTGATGAGGCTATTTCTTTG 780
QY 785 GTTTCGAGAGAGAGAGACAAGAAAGTATGAAAGAGAAAGAGAGTGGACATTTG 844
DB 781 GTTTCGAGAGAGAGAGACAAGAAAGTATGAAAGAGAAAGAGAGTGGACATTTG 840
QY 845 TCGGGAAGCTCTTAATATATGCCCCCATTTCTGAGAGAACTAGATGAGACAAATCCC 904
DB 841 TCGGGAAGCTCTTAATATATGCCCCCATTTCTGAGAGAACTAGATGAGACAAATCCC 900
QY 905 TCACACTAATATGAGAACTTAAGAAAGATCCAGAAATATAGGTTTATCCAGTGTGA 964
DB 901 TCACACTAATATGAGAACTTAAGAAAGATCCAGAAATATAGGTTTATCCAGTGTGA 960
QY 965 AATACGGAAGAAAGATGAGAAATCCCACTACGTCTCAGATGCCAGACCAAGGCT 1024

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Qy	1025	ATTGGCTATGAGATGTATCTAGACAGCAGTGCATCCCTAAGTCTGTGCTCA	1080
Db	1021	ATTGGCTATGAGATGTATCTAGACAGCAGTGCATCCCTAAGTCTGTGCTCA	1076

Search completed: October 28, 2004, 04:50:12
Job time : 1287 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 07:59:30 ; Search time 1268 Seconds
(without alignments)
10934.571 Million cell updates/sec

Title: US-09-745-605-1

Perfect score: 2704
Sequence: 1 ggaagtgcttcattcattcgcgttgcgttcgagagcaatattgctgtcccaacat 2704

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1369.4	50.6	1412	10	US-09-966-262-15
5	1369.4	50.6	1412	10	US-09-983-966-15
6	1369.4	50.6	1412	14	US-10-059-395-15
7	1369.4	50.6	1412	14	US-10-143-090-15
8	1082	40.0	1082	16	US-10-262-839-109
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41	1076	39.8	1076	10	US-09-998-156-252	Sequence 252, App
42	1076	39.8	1076	10	US-09-990-437-252	Sequence 252, App
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45	1076	39.8	1076	10	US-09-997-573-252	Sequence 252, App

ALIGNMENTS

RESULT 1

US-09-745-605-1

Sequence 1, Application US/09745605

Patent No. US20020123617A1

GENERAL INFORMATION:

APPLICANT: Starling, Gary C.

TITLE OF INVENTION: NOVEL IMMUNOGLOBIN SUPERFAMILY MEMBERS APEX-1, APEX-2, AND USES THEREOF

FILE REFERENCE: DB13NP

CURRENT APPLICATION NUMBER: US/09/745,605

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/172,025

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 2704

TYPE: DNA

ORGANISM: Homo sapiens

US-09-745-605-1

Query Match	100.0%	Score 2704;	DB 9;	Length 2704;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 2704;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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541 TGGGGCAAGCAGCAATGATGCCATATAGGGTCCATCCCTCCCATCTCTGGAAGTGG 600
601 GAGAAAGTATATGACCTTATCTGCGTTGCGAGAACCTGTGACAGAAATTTCTCA 660
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661 GCGCCATCTCTGCGAGAAAGCTGTGGAAGTGTCTGTGAACCAATTTCTCATGG 720
661 GCGCCATCTCTGCGAGAAAGCTGTGGAAGTGTCTGTGAACCAATTTCTCATGG 720
721 TCCCTCGTGTCTCCTGTTGTTGTTGTCCTGCTCAAGTCTTTGACTGGGGCTATTTTC 780
721 TCCCTCGTGTCTCCTGTTGTTGTTGTCCTGCTCAAGTCTTTGACTGGGGCTATTTTC 780
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Qy 2341 CTGAGTACAGTCTGAGCAGTAAATGAAACATCCCTACCAACAGAGCTCACCATC 2400
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Qy 2401 TCTTATATCTTAAGTGAAGAAACATGGGGAAGGGGAAGGGAATGGCTCTTTGATATGT 2460
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Qy 2461 TCCCTGACGATATCTTGAATGAGACTCCCTACCAAGTATGAAAGTGTGAAAACCT 2520
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Db 2521 TAATTAACAAATGCTGTTGGGCAAGAAATGGGAATGAGATTAATCTTCTCAGAAAAGCA 2580
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Db 2641 TCTTCTTACTATCTTAAATAAACAGATTTGTGAGATTCACATTAATAAAAAAAAAAAAA 2700
Qy 2701 AAAA 2704
Db 2701 AAAA 2704

RESULT 2

US-10-198-846-13630
; Sequence 13630, Application US/10198846
; Publication No. US2003099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinhilber, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FASTA/Seq for Windows Version 4.0
; SEQ ID NO 13630
; LENGTH: 1966
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..2..1966
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13630

Query Match 62.9%; Score 1701.4; DB 14; Length 1966;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 11; Indels 9; Gaps 5;

Qy 912 AATGAACAAATCTTAAGAAAGATCCAGCAAAATACGGTTTACTGCTGAGAAATACCG 971
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Qy 972 AAAAAAGTGAAGAAATCCCACTCACTGCTCAAGTGCAGACACCAAGGCTATTTGCC 1031
Db 193 AAAAAAGTGAAGAAATCCCACTCACTGCTCAAGTGCAGACACCAAGGCTATTTGCC 252
Qy 1032 TATGAGATGTTATCTAGACAGAGTCACTCCCTAAGTCTGTCTCAAAAAAAAAACA 1091
Db 1032 TATGAGATGTTATCTAGACAGAGTCACTCCCTAAGTCTGTCTCAAAAAAAAAACA 1091

Db 253 TATGAGATGAGTATGAGACAGAGTCACTCCCTAAGTCTGTCTCAAAAAAAAAACA 312
Qy 1092 ATTCTGGGCCCCAAGAAACAAATCAGAAAGATTCAGATTTAGTAG--AAATCAGG 1150
Db 313 ATTCTGGGCCCCAAGAAACAAATCAGAAAGATTCAGATTTAGTAGAAACATCAGG 372
Qy 1151 AAGAAATGAAGAGTGAATCTTTTCCAGAGTAAATATCTGATGCTCTTTAGATTT 1210
Db 373 AAGAAATGAAGAGTGAATCTTTTCCAGAGTAAATATCTGATGCTCTTTAGATTT 432
Qy 1211 AAGATTTGTAATTCATTCATCTGAGAAATCTCTCAACCCAGAAAGTTTATCAC 1270
Db 433 AAGATTTGTAATTCATTCATCTGAGAAATCTCTCAACCCAGAAAGTTTATCAC 492
Qy 1271 TTGATCCCAAAATGAGATTTGTAATGTCAGCAAAACCTTAATAAAAGTCTTTGAAGTAT 1330
Db 493 TTGATCCCAAAATGAGATTTGTAATGTCAGCAAAACCTTAATAAAAGTCTTTGAAGTAT 552
Qy 1331 TCCATTAAGAAATGTAATGCAAGTCAACATATTAATGACAGCTGTTGATTAATGAT 1390
Db 553 TCCATTAAGAAATGTAATGCAAGTCAACATATTAATGACAGCTGTTGATTAATGAT 612
Qy 1391 GAGTCAAGTCAAGTCTGAGATTTGATTCATTCATCCAGAGCTTGATGTCAGATTAATAC 1450
Db 613 GAGTCAAGTCAAGTCTGAGATTTGATTCATTCATCCAGAGCTTGATGTCAGATTAATAC 672
Qy 1451 CAGAGTCTTGTCTACAGAGGAGGCAAGAAACCAAAACAGACAGAAAGTCCAGCAAGAG 1510
Db 673 CAGAGTCTTGTCTACAGAGGAGGCAAGAAACCAAAACAGACAGAAAGTCCAGCAAGAG 732
Qy 1511 CAGATGCACTGCAAAATAATGATGATTAATTTGGCTCTTAATAATATGAGCCAGACT 1570
Db 733 CAGATGCACTGCAAAATAATGATGATTAATTTGGCTCTTAATAATATGAGCCAGACT 792
Qy 1571 ATGCTGAGCTTACATTAATTTGTCAGACGCTGCTGCTGCTCCTGATGAATTTGCTCCAA 1630
Db 793 ATGCTGAGCTTACATTAATTTGTCAGACGCTGCTGCTGCTCCTGATGAATTTGCTCCAA 852
Qy 1631 TGAATGAATCTTCTTATGAGAGCTGTCAGAGGCTGACCAAGATTTCCAGAGGCCCA 1690
Db 853 TGAATGAATCTTCTTATGAGAGCTGTCAGAGGCTGACCAAGATTTCCAGAGGCCCA 912
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Db 973 ACCATGTTTGGCAGATTAATAATGAGACACAGAAAGTGTGATGAGCCCAAGACAAGA 1032
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Db 1033 CCTCCAGCCAGGCTTCAATTTATGCACTTGTGCTGCAAAAGAAAGTCTAGGTTTAAAGC 1092
Qy 1871 TGTGCCAGAAACCATCCCAATAAAGAGACCGAGTCTGAAGTCAATTTGTAATCTAGTGT 1930
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Qy 1931 AAGAGACTTGAAGTCAAGCAGTGAAGCTGTGTGGGAGCAGGGGGGAGTGGGTACTTTGTA 1990
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Qy 2111 GAGGTCAAGAGTTCAAGACCAAGCTGAGCAATGCTGAACCCCATCTCTAATAAGAT 2170
Db 1330 GAGGTCAAGAGTTCAAGACCAAGCTGAGCAATGCTGAACCCCATCTCTAATAAGAT 1389

LOCATION: (1369)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1397)
OTHER INFORMATION: n equals a,t,g, or c
US-09-966-262-15

Query Match 50.6%; Score 1369.4; DB 10; Length 1412;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1384; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

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QY 616 CCTTCATCTGCGTGGCAGGAACCTGTGACGAGAACTTCTCAGAGCCCATCTTGGCA 675
DB 2 CCTTCATCTGCGTGGCAGGAACCTGTGACGAGAACTTCTCAGAGCCCATCTTGGCA 61
QY 676 GGAAGCTGTGAGAGGTGCTGATGACCCAGATTCCTCAATGTCCTCTGTCTCC 735
DB 62 GGAAGCTGTGAGAGGTGCTGATGACCCAGATTCCTCAATGTCCTCTGTCTCC 121
QY 736 TGTGTGCGCCCTCTCTGCTCAGTCTCTTGTACTGTGGGCTAATTTCTTGGTTCTGAGA 795
DB 122 TGTGTGCGCCCTCTCTGCTCAGTCTCTTGTACTGTGGGCTAATTTCTTGGTTCTGAGA 181
QY 796 GAGAGACACAGAGATGATTAAGAGAGAGAGAGAGAGATGACATTTGTCGGAAATCTC 855
DB 182 GAGAGACACAGAGATGATTAAGAGAGAGAGAGAGATGACATTTGTCGGAAATCTC 241
QY 856 CTAACTATGCCCCCTTCTGAGAGAGACAGAGATGACCAATCCCTCACATTA 915
DB 242 CTAACTATGCCCCCTTCTGAGAGAGACAGAGATGACCAATCCCTCACATTA 301
QY 916 GAACATCTTAAAGAGAGATCCAGCAATATACGTTTACTCACTGTGAAATACCGAAA 975
DB 302 GAACATCTTAAAGAGAGATCCAGCAATATACGTTTACTCACTGTGAAATACCGAAA 361
QY 976 AGATGAAAATCCCACTACCTGCTCAGATGCGACACACCAAGGCTAATTTGCTATG 1035
DB 362 AGATGAAAATCCCACTACCTGCTCAGATGCGACACACCAAGGCTAATTTGCTATG 421
QY 1036 AGATGTTATCTAGACAGAGTCACTCCCTTAAGTCTGCTCAAAAAAACAATTC 1095
DB 422 AGATGTTATCTAGACAGAGTCACTCCCTTAAGTCTGCTCAAAAAAACAATTC 481
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DB 482 TCGGCCCAAGAAACAATCAGAGAAATTCAGTATTTGACTAGAAATCAAGAGAA 541
QY 1156 TGAAGAACTTGAATTTTCCAGATTAATTAATCTGATGCTTTTGAATTTAAG 1215
DB 542 TGAAGAACTTGAATTTTCCAGATTAATTAATCTGATGCTTTTGAATTTAAG 601
QY 1216 TTGTTATTCATTCACCTGCTGAGAAATCTCCCAAGGCTTAATCACTCAT 1275
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QY 1276 CCCAAAATGGAGTTGTGATGTCAGCAAAACATTAATAAAGTCTTAGAATATTCCTA 1335
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DB 1202 AGCCAGGCTTCATTTATGACCTTGTGTCACAAAAGATCTAGGTTTAAAGGCTGTGC 1260
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DB 1261 CAGAACCATCCCAATTAAGAGACCGAGTCTGAATGATCAATTTGAATCTAGTATGAGAG 1320
QY 1936 ACTTGAGTCAAGGCGAGTGAAGTGTGAGGCGACGAGGCGAGTGTGATTAACCTT 1995
DB 1321 ACTTGAGTCAAGGCGAGTGAAGTGTGAGGCGACGAGGCGAGTGTGATTAACCTT 1380
QY 1996 TAAAGATGTTAATTCAT 2013
DB 1381 TAAAGATGTTAATTCAT 1398
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RESULT 5
US-09-983-966-15
Sequence 15, Application US/09983966
Publication No. US20030060619A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
CURRENT APPLICATION NUMBER: US/09/983,966
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: US 60/041,277
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/042,344
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,276
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,281
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/048,094
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,350
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,188
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,135
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/050,937
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,187
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,099
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,352
PRIOR FILING DATE: 1997-05-30

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; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
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; PRIOR FILING DATE: 1997-05-30
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: (1362)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1369)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1397)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-983-966-15

Query Match      50.6%; Score 1369.4; DB 10; Length 1412;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1386; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 616 CCTTCACTGCGTGGCCAGAACCTGTGACAGAACTTCTCAAGCCCATCTTGCCA 675
Db 2 CTTTCACTGCGTGGCCAGAACCTGTGACAGAACTTCTCAAGCCCATCTTGCCA 61
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Db 62 GGAAGCTCTGTGAAGTGTGCTGATGATGACCAAGTTCTTCAAGTCTCTGTTGCC 121
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QY 916 GAACAATCTTAAGAGAGATCCAGCAATATCGGTTTACTCACTGTTGAATACCGGAAA 975
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QY 976 AGATGAGAAATCCCACTCACTGCTCAAGTGCAGACACACCAAGGCTATTGCTATG 1035
Db 362 AGATGAGAAATCCCACTCACTGCTCAAGTGCAGACACACCAAGGCTATTGCTATG 421
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Db 482 TCGGCCCAAGAAACAAATCAGAAAGATTCACTGATTTGACTAGAAACATCAAGAGAA 541
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Db 1142 GTTTGGCAATACTAATTAAGAGACACAGAGTGTGATGCCCCAAGAGCAAGGACTCC 1201
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Db 1261 CAGAACCATCCCAATTAAGAGACGAGTCTGAAGTCAATTTGAATCTAGTGTAGAG 1320
QY 1936 ACTTGAAGTCAAGCATGAGTGTGTGGGACACGGGGGGCAGTGGTACTTGTAAACCTT 1995
Db 1321 ACTTGAAGTCAAGCATGAGTGTGTGGGACACGGGGGGCAGTGGTACTTGTAAACCTT 1380
QY 1996 TAAAGATGTTAATTCAT 2013
Db 1381 TAAAGATGTTAATTCAT 1398
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RESULT 6
US-10-059-395-15
; Sequence 15, Application US/10059395

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; Publication No. US20030018180A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/10/059,395
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/966,262
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
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; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1362)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1369)

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; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1397)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-059-395-15

Query Match      50.6%; Score 1369.4; DB 14; Length 1412;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1384; Conservative      2; Mismatches 11; Indels 1; Gaps 1;

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676 GGAAGCTCTGTGAAGGTGCTGTATGACCCAGATTCCTCATGTCTCTGTCTCC 735
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736 TGTGTGTGCTCTCTGTCTGTATGATCTTTGTATCTGAGGCTATTTTGTGTGAAGA 795
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122 TGTGTGTGCTCTCTGTCTGTATGATCTTTGTATCTGAGGCTATTTTGTGTGAAGA 181
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796 GAGAGAGACAAAGAAAGTATGATGAGAGAAAGAAAGAGAGTGAATTTGTGGGAAATCC 855
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242 CTAACATATGCCCCCATTTCTGGAGAGAAACAGAGTACGACATCCCTCACATAATA 301
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422 AGAATGTTATCTAGACAGACAGTGCATCCCTTAAGTCTGTCTCAAAAAAACAATTC 481
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1096 TCGGCCCAAGAAACAATCAGAGAAATTCAGTATTTGACTAGAAACATCAAGAGAA 1155
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662 CCCAAATATGGATTTGATATGTCAGCAAAACCATTAATAAAGTCTTGAAGTATTCCTA 721
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782 CAGTCAAGTGTGAGATTTTCAATTCACAGGCTGTGATGTCAGATTTTACCAAGA 841
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1456 GTCTTGCTACAGAGAGGCAAGAGACCAAAACAGACAGCAAGTTCAGACAGAGCAT 1515
;
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QY 1936 ACTTGGAGTGAAGGAGTGAAGTGTGGGCGACGGGGGCGAGTGGGTACTTGTAAAGCTT 1995
DB 1321 ACTTGGAGTGAAGGAGTGAAGTGTGGGCGACGGGGGCGAGTGGGTACTTGTAAAGCTT 1380
QY 1996 TAAAGATGTTAAATTCAT 2013
DB 1381 TAAAGATGTTAAATTCAT 1398

RESULT 7
US-10-143-090-15
; Sequence 15, Application US/10143090
; Publication No. US20030069406A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/10/143, 090
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1362)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1369)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1397)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-143-090-15

Query Match 50.6%; Score 1369.4; DB 14; Length 1412;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1384; Conservative 2; Mismatches 11; Indels 1; Gaps 1;
QY 616 CTTTCATCTGCGTTGCGAGGAAACCTCTGTACAGCAGAACTTCTCAAGCCCATCTTGCCA 675
DB 2 CTTTCATCTGCGTTGCGAGGAAACCTCTGTACAGCAGAACTTCTCAAGCCCATCTTGCCA 61

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Db 841 TGTGGGAACTCTTAACATATGCCCCATTCTGAGAGAACACAGATGACACATC 900
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Db 901 CCTCACATATAGAACATCTTAAGAGATCAGCAATACGTTTACTCCACTGTG 960
Qy 963 GAAATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGACACCAAG 1022
Db 961 GAAATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGACACCAAG 1020
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Qy 1083 AA 1084
Db 1081 AA 1082

RESULT 9
US-09-989-722-252
Sequence 252, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botsstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertschen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C3
CURRENT APPLICATION NUMBER: US/09/989, 722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28

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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
Query Match 39.8%; Score 1076; DB 9; Length 1076;
Best Local Similarity 100.0%; Pred.No. 1.5e-294;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 65 CACCCCTCATATATCTTGGGACGCTCAAGGCTCAGAGCTTGGAGCCGCTGAAGA 124
DB 61 CACCCCTCATATATCTTGGGACGCTCAAGGCTCAGAGCTTGGAGCCGCTGAAGA 120
QY 125 GCTGGTGGGTTCCGTTGGTGGGCGGTGACTTTCCCTGGAAGTCAAGTAAAGCAAGT 184
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QY 185 TGAATCTATTTGTTGGAAGCTTGAACAACCCCTTGTCACTATACAGCCGAAGGGGG 244
DB 181 TGAATCTATTTGTTGGAAGCTTGAACAACCCCTTGTCACTATACAGCCGAAGGGGG 240
QY 245 CACTATCATATAGGACCCCAAAATGTAATAGGAGAGAGTGAAGTCCCAAGATGAGGGCTA 304
DB 241 CACTATCATATAGGACCCCAAAATGTAATAGGAGAGAGTGAAGTCCCAAGATGAGGGCTA 300
QY 305 CTCCTGGAAGCTCAGCAAACTGGAAGAATGACTCAGGATCTACTATGTGGGATATA 364
DB 301 CTCCTGGAAGCTCAGCAAACTGGAAGAATGACTCAGGATCTACTATGTGGGATATA 360
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DB 361 CAGCTCATATCTCCAGCAGCCCTCCACCAAGAGTACGTGCTGATGTGTACAGACACTT 420
QY 425 GTCAAGGCTTAAGTCAACATGGGTTCTGAGAGCAATAGGACCTGTGTGACCA 484
DB 421 GTCAAGGCTTAAGTCAACATGGGTTCTGAGAGCAATAGGACCTGTGTGACCA 480
QY 485 TCTGACATGCTGCAATGGAACATGGGAAAGAGATGATTTATACCTGGAAGCCCTGGG 544
DB 481 TCTGACATGCTGCAATGGAACATGGGAAAGAGATGATTTATACCTGGAAGCCCTGGG 540
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DB 721 CCTGTGTTCTCTGTGGTGGCCCTCTCTGCTCAGTCTTTGTATGAGGGCTATTTCTTTG 780
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DB 841 TCGGAAACTCTTAATATATGCCCCATTTGAGAGAGAACAGAGTACGACATATCCC 900
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Db 961 AATAACCAAAAAGATGGAATATCCCACTACATGCTCTACAGATGCCACACACCAAGGCT 1020
Qy 1025 ATTTGCTATGAGATGTATCTAGACAGAGATGCACTCCCTTAAGTCTGTGCTCA 1080
Db 1021 ATTTGCTATGAGATGTATCTAGACAGAGATGCACTCCCTTAAGTCTGTGCTCA 1076

RESULT 10
US-09-989-723-252
; Sequence 252, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoves, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
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; APPLICANT: Pan, James
; APPLICANT: Pion, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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65 PRIOR FILING DATE: 1998-07-07
66 PRIOR APPLICATION NUMBER: 60/092182
67 PRIOR FILING DATE: 1998-07-09

Query Match 39.8%; Score 1076; DB 9; Length 1076;
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61 CACCCCTCATATATATCTTTGGACACTCAGAGGGTCACAGCTCTGGACCCGTAAAGA 120
125 GCTGTGCGTTCCTGTGGTGGGGCGGTAGACTTTCCTTGAAGTCCAAAGTAAAGCAAGT 184
121 GCTGTGCGTTCCTGTGGTGGGGCGGTAGACTTTCCTTGAAGTCCAAAGTAAAGCAAGT 180
185 TGACTCTATTTGCTTGAGACTTTCACACACACACCCCTTGTCTACCATACAGCCAGAGGGG 244
181 TGACTCTATTTGCTTGAGACTTTCACACACACACCCCTTGTCTACCATACAGCCAGAGGGG 240
245 CACTATCATATGAGACCCAAATCGTAATAGGAGAGATAGACTTCCAGATGGAGGCTA 304
241 CACTATCATATGAGACCCAAATCGTAATAGGAGAGATAGACTTCCAGATGGAGGCTA 300
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301 CTCCCTGAAGCTCAGCAAACTGAGAGAGATGACTCAGAGATCTACTATGTGGGATATA 360
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361 CAGCTCATACTCCAGCAGCCCTCCACCAGAGATGACTGCTGCAATGCTACAGCACCT 420
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781 GTTTCGAAGAGAGAGAGAGAGAGAGATGATTAAGAGAGAGAGAGAGAGATTTG 840
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905 TCACATATATGAGACATCTTAAGAGAGATGATGAGAGAGATGATTTG 964
901 TCACATATATGAGACATCTTAAGAGAGATGATGAGAGAGATGATTTG 960
965 AATACCGAAAAAGATGAAAAATCCCACTGCTGACAGATGAGAGAGAGATTTG 1024
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1021 ATTGCTATGAGATGATTTATCTAGACAGAGTGAATCTCCCTAAGTCTGCTCA 1076

RESULT 11

US-09-989-279-252
Sequence 252, Application US/09989279
Patent No. US20020072496A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertschen, Mary B.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
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PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/090355

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P230P1C65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
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;; PRIOR FILING DATE: 1998-07-09

Query Match 39.8%; Score 1076; DB 9; Length 1076;
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Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Tumas, Daniel

APPLICANT: Matanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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; CURRENT APPLICATION NUMBER: US/09/989,732
; PRIOR FILING DATE: 2001-11-19
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DB 241 CACTATCATATGAGACCAATTCATATAGGAGAGATGATGATGATGATGATGATGAT 300
QY 305 CTCCTGGAAGTCAGCAAACTGAGAAAGATGATGATGATGATGATGATGATGATGAT 364
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QY 365 CAGCTCATATCTCCAGAGCCCTCCACCCAGAGATGATGATGATGATGATGATGAT 424
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DB 421 GTCAAAAGCTTAAGTACATAGGTTGTGAGAGCAATAGATGATGATGATGATGATGAT 480
QY 485 TCTGATATCTGATGAGAACTGAGGAGAGATGATGATGATGATGATGATGATGATGAT 544
DB 481 TCTGATATCTGATGAGAACTGAGGAGAGATGATGATGATGATGATGATGATGATGAT 540
QY 545 GCAAGAGCAATGAGTCCCATATATGATGATGATGATGATGATGATGATGATGATGAT 604
DB 541 GCAAGAGCAATGAGTCCCATATATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 605 AAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664
DB 601 AAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 665 CATCTTGCAGAGAGCTGATGAGAGTCTGATGATGATGATGATGATGATGATGATGAT 724
DB 661 CATCTTGCAGAGAGCTGATGAGAGTCTGATGATGATGATGATGATGATGATGATGAT 720
QY 725 CCGTGTCTCTCTGTGTGTGTCCTCTGTCTCAATCTCTTGTATGAGGGCTATTTCTT 784
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DB 721 CCTGTCTCTCTGTGTGTGTCCTCTGTCTCAATCTCTTGTATGAGGGCTATTTCTT 780
QY 785 GTTCTGAGAGAGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATG 844
DB 781 GTTCTGAGAGAGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATG 840
QY 845 TCGGAAATCTCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 904
DB 841 TCGGAAATCTCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 905 TCACTATATGAGAAATCTTAAGAGATGATGATGATGATGATGATGATGATGATGATG 964
DB 901 TCACTATATGAGAAATCTTAAGAGATGATGATGATGATGATGATGATGATGATGATG 960
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DB 961 AATACCGAAAAGATGAGAAATCCCACTGATGATGATGATGATGATGATGATGATGAT 1020
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DB 1021 ATTTGCTATGAGAAATGTTATCTAGACAGAGTGAATCCCTAAGTCTTGCTCA 1076
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RESULT 15
US-09-991-073-252
; Sequence 252, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Geider, Hanspeter
; APPLICANT: Gerilsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Auecin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Steward, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C15
; CURRENT APPLICATION NUMBER: US/09/991,073
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
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[illegible]

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 39.8%; Score 1076; DB 9; Length 1076;
Best Local Similarity 100.0%; Pred. No. 1.5e-294;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 GCTGTGCGGTTCCGTTGGTGGGCGGTGACTTCCCTGGAAGTCCAAAGTAAAGCAAGT 180
QY 185 TGACTTATTTGTGAGACCTTCAACACAAACCCCTTGTTCACCATACAGCCAGAGAGGAG 244
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QY 545 GCAAGCAGCCAAATGAGTCCCATATATGGGTCCATCTCCCATCTCTGAGATGGGAGA 604
DB 541 GCAAGCAGCCAAATGAGTCCCATATATGGGTCCATCTCCCATCTCTGAGATGGGAGA 600
QY 605 AAGTGAATAGACCTTATCTGCGTGTGCAAGAACCTGTGAGCAAACTTCTCAAGCCC 664
DB 601 AAGTGAATAGACCTTATCTGCGTGTGCAAGAACCTGTGAGCAAACTTCTCAAGCCC 660
QY 665 CATCTTGGCAGGAAGCTCTGTGAAGGTCTGTGATGACCCAGATTCTCCATGCTCT 724
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QY 725 CCTGTGTCTCTGTGTGGTGGCCCTCTGTGCTCACTCTTTGTATCTGGGGCTAATTTCTTTG 784
DB 721 CCTGTGTCTCTGTGTGGTGGCCCTCTGTGCTCACTCTTTGTATCTGGGGCTAATTTCTTTG 780
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DB 781 GTTTCTGAAGAGAGAGACAAAGAGATACATTGAAGAGAGAGAGAGTGAATTTG 840
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DB 961 AATACGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGACACCAAGGCT 1020
QY 1025 ATTTGCTATAGAAATGTTATCTAGACAGCAGTGCATCCCTTAAGTCTGTGCTCA 1080
DB 1021 ATTTGCTATAGAAATGTTATCTAGACAGCAGTGCATCCCTTAAGTCTGTGCTCA 1076

Search completed: October 28, 2004, 13:30:12
Job time : 1274 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: October 28, 2004, 03:57:30 ; Search time 222 Seconds

(without alignments)
8657.537 Million cell updates/sec

Title: US-09-745-605-1

Perfect score: 2704
Sequence: 1 ggaagcgcctcttcacg.....aaaaaaaaaaaaaaaaa 2704

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing filter 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	890.2	32.9	921	4	US-09-023-655-401 Sequence 401, App
2	375.6	13.9	435	4	US-09-513-999C-21312 Sequence 21312, A
3	331.6	12.3	344	4	US-09-513-999C-395 Sequence 395, App
4	194.4	7.2	5037	4	US-09-705-299-13 Sequence 13, App1
5	190.8	7.1	4773	3	US-08-884-324-9 Sequence 9, App1
6	190.8	7.1	4773	4	US-09-479-862-9 Sequence 9, App1
7	190.8	7.1	11464	3	US-08-884-324-13 Sequence 13, App1
8	190.8	7.1	11464	4	US-09-479-862-13 Sequence 13, App1
9	190.8	7.1	28994	3	US-08-884-324-14 Sequence 14, App1
10	190.8	7.1	28994	4	US-09-479-862-14 Sequence 14, App1
11	189.4	7.0	114793	4	US-10-148-806-3 Sequence 3, App1
12	188.4	7.0	39982	4	US-09-820-924-3 Sequence 3, App1
13	188.4	7.0	39982	4	US-10-369-626-3 Sequence 3, App1
14	187.4	6.9	162450	3	US-09-539-882-1 Sequence 1, App1
15	187.4	6.9	319608	4	US-09-539-882-1 Sequence 1, App1
16	187.4	6.9	319608	4	US-09-679-409-1 Sequence 1, App1
17	186.4	6.9	55298	4	US-09-491-356C-1 Sequence 1, App1
18	185.4	6.9	11811	3	US-09-078-294-7 Sequence 7, App1
19	185.2	6.8	17000	4	US-09-548-797B-7 Sequence 7, App1
20	184.8	6.8	9365	3	US-09-608-285A-8 Sequence 8, App1
21	184.8	6.8	9365	3	US-09-350-836B-8 Sequence 8, App1
22	184.8	6.8	9365	4	US-09-370-265-8 Sequence 8, App1
23	184.8	6.8	9365	4	US-09-557-800C-8 Sequence 8, App1
24	184.8	6.8	9365	4	US-09-370-625A-8 Sequence 8, App1
25	184.8	6.8	14747	3	US-09-608-285A-42 Sequence 42, App1
26	184.8	6.8	14747	4	US-09-557-800C-42 Sequence 42, App1
27	184.8	6.8	15977	3	US-09-608-285A-59 Sequence 59, App1

28	184.6	6.8	148567	4	US-09-801-876B-3 Sequence 3, App1
29	184.6	6.8	148567	4	US-10-254-869-3 Sequence 3, App1
30	183.4	6.8	2921	3	US-08-618-100B-4 Sequence 4, App1
31	183.2	6.8	55298	4	US-09-491-356C-1 Sequence 1, App1
32	183	6.8	70000	4	US-09-851-896-3 Sequence 3, App1
33	182.6	6.8	81001	4	US-09-750-580-1 Sequence 1, App1
34	182.4	6.7	466	4	US-09-621-976-18219 Sequence 18219, A
35	182	6.7	64467	4	US-09-803-671B-3 Sequence 3, App1
36	181.8	6.7	14684	4	US-09-536-059-1 Sequence 1, App1
37	181.8	6.7	80246	3	US-09-078-294-4 Sequence 4, App1
38	181.8	6.7	80595	3	US-09-078-294-3 Sequence 3, App1
39	181.6	6.7	489	4	US-09-621-976-17265 Sequence 17265, A
40	181.6	6.7	111282	3	US-09-754-250-3 Sequence 3, App1
41	181	6.7	66933	4	US-09-544-398B-11 Sequence 11, App1
42	181	6.7	66933	4	US-09-543-771-11 Sequence 11, App1
43	181	6.7	72049	4	US-09-544-398B-9 Sequence 9, App1
44	181	6.7	72049	4	US-09-543-771-9 Sequence 9, App1
45	180.8	6.7	106746	4	US-09-326-402C-1 Sequence 1, App1

ALIGNMENTS

RESULT 1
US-09-023-655-401
Sequence 401, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 401:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THPLPLB02
CLONE: 156352
US-09-023-655-401

Query Match 32.9%; Score 890.2; DB 4; Length 921;

Best Local Similarity 99.5%; Pred. No. 2.8e-254;
Matches 914; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
Db 1123 TTCCGATTTGATGAAACATCAAGAA-GAATGAAGAAGCTTACCTTTTCCAGGA 1181
1 TTCCGATTTGATGAAACATCAAGAA-GAATGAAGAAGCTTACCTTTTCCAGGA 60
Qy 1182 TAAATATCTGATGCTTCTTATTAAGATTGAATTCATTCACCTGCTGAGA 1241
Db 61 TAAATATCTGATGCTTCTTATTAAGATTGAATTCATTCACCTGCTGAGA 120
Qy 1242 ATCTCTCAAAACCAAGGTTTAACTTCACTTCCCAAAAATGGGATTGTGATGCTAG 1301
Db 121 ATCTCTCAAAACCAAGGTTTAACTTCACTTCCCAAAAATGGGATTGTGATGCTAG 180
Qy 1302 CAACCATTAATAAAGGCTTAGAATTTCTATGAATAATGAATGAAGGTCACACA 1361
Db 181 CAACCATTAATAAAGGCTTAGAATTTCTATGAATAATGAATGAAGGTCACACA 240
Qy 1362 TATTAATGACAGCTGTGATTAATGATGCTCCAGGTCAGTGTCTGAGTTTCATTCC 1421
Db 241 TATTAATGACAGCTGTGATTAATGATGCTCCAGGTCAGTGTCTGAGTTTCATTCC 300
Qy 1422 ATCCGAGGCTTGATGATGCTGAGATTATCCAGAGTCTTGTCTACGAGGCGCAAGAA 1481
Db 301 ATCCGAGGCTTGATGATGCTGAGATTATCCAGAGTCTTGTCTACGAGGCGCAAGAA 360
Qy 1482 CCAAAACAGACAGCAAGTCCAGACAGAGAGATGACCTGACAAATAATGATGATTA 1541
Db 361 CCAAAACAGACAGCAAGTCCAGACAGAGAGATGACCTGACAAATAATGATGATTA 420
Qy 1542 TTGGCTCTATTAATCTATGCTCCAGACATATGCTGACTTACCTAATTTGCTCAGAG 1601
Db 421 TTGGCTCTATTAATCTATGCTCCAGACATATGCTGACTTACCTAATTTGCTCAGAG 480
Qy 1602 CTGTCTGCTCTATGAAATTTGGTCCAAATGAATGAATGACTTTCATGAGGCTGTAG 1660
Db 481 CTGTCTGCTCTATGAAATTTGGTCCAAATGAATGAATGACTTTCATGAGGCTGTAG 540
Qy 1661 CAGGCTGACACAGATTTCCAGAGGCGCAGGTTGATTCACAGGACTTGAAGGTCAA 1720
Db 541 CAGGCTGACACAGATTTCCAGAGGCGCAGGTTGATTCACAGGACTTGAAGGTCAA 600
Qy 1721 GTTCACAAAAGATGAAGATCAGGATGCTGACCATTTTGGCAGATATATATGAGAC 1780
Db 601 GTTCACAAAAGATGAAGATCAGGATGCTGACCATTTTGGCAGATATATATGAGAC 660
Qy 1781 ACAGAGTGTGATGCTGCTCCAGAGCAAGACCTCCAGGCGGTTCAATTAATGACCTGT 1840
Db 661 ACAGAGTGTGATGCTGCTCCAGAGCAAGACCTCCAGGCGGTTCAATTAATGACCTGT 720
Qy 1841 GCTGCAAAAAGAAAGCTAGGTTTAAAGGCTGAGCAAGAACCATCCAAATAAGAGAC 1900
Db 721 GCTGCAAAAAGAAAGCTAGGTTTAAAGGCTGAGCAAGAACCATCCAAATAAGAGAC 780
Qy 1901 GAGTCTGAAGTCACTTGTAAATCTATGATGAGAGACTTGAAGTCAAGGAGTGAAGCTG 1960
Db 781 GAGTCTGAAGTCACTTGTAAATCTATGATGAGAGACTTGAAGTCAAGGAGTGAAGCTG 840
Qy 1961 TGGGGGACGGGGGCGGCTGCTTAAACCTTTAAAGATGCTTAATTCATTCAATAG 2020
Db 841 TGGGGGACGGGGGCGGCTGCTTAAACCTTTAAAGATGCTTAATTCATTCAATAG 900
Qy 2021 ATATTATTAAAGACTAC 2039
Db 901 ATATTATTAAAGACTAC 919

RESULT 2
US-09-513-999C-21312
; Sequence 21312, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59. US2. REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 21312
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-21312

Query Match 13.9%; Score 375.6; DB 4; Length 435;

Best Local Similarity 97.3%; Pred. No. 1.9e-101;
Matches 426; Conservative 0; Mismatches 4; Indels 8; Gaps 4;

Qy 1857 CTAGGTTTAAAGCTGTGCTCCAGAACCATCCCAATTAAGACCGAGTCTGAAGTCACAT 1916
Db 1 CTAGGTTTAAAGCTGTGCTCCAGAACCATCCCAATTAAGACCGAGTCTGAAGTCACAT 60
Qy 1917 TGTAAATCTAGTGTGAGAGACTTGGAGTCAAGGAGTGAAGTCTGTGGGCGCAGGAGCA 1976
Db 61 TGTAAATCTAGTGTGAGAGACTTGGAGTCAAGGAGTGAAGTCTGTGGGCGCAGGAGCA 120
Qy 1977 GTGGTACTTGTAAACCTTTAAAGATGCTTAATTCATTCAATGATTAATTAAGAAC 2036
Db 121 GTGGTACTTGTAAACCTTTAAAGATGCTTAATTCATTCAATGATTAATTAAGAAC 179
Qy 2037 TACTATGGGCGCCGCGCATGCTGCTCAGACCTGTAATCCAGACATTTGGAGGCGCAGG 2096
Db 180 --CTATGGGCGCCGCGCATGCTGCTCAGACCTGTAATCCAGACATTTGGAGGCGCAGG 237
Qy 2097 TGGGTGGTCACTAGGCTCAGAGGTCAGAGTCAAGACCGCTGGCCAACTAGTGAACCCCA 2156
Db 238 TGGGTGGTCACTAGGCTCAGAGGTCAGAGTCAAGACCGCTGGCCAACTAGTGAACCCCA 297
Qy 2157 TCTCTACTAAAGAT--CAAAATTTGCTGAGCGTGTGTGTGACCTGT-ATCCAGCTA 2213
Db 298 TCTCTACTAAAGATCAAAAATTTGCTGAGCGTGTGTGTGACCTGTATATCCAGCTA 357
Qy 2214 CTCGAGAGGCCAAGGATGAGAAATGCTTGAACCTGG--AGTGAAGTTGCAAGTGAAGCTG 2271
Db 358 CTCGAGAGGCCAAGGATGAGAAATGCTTGAACCTGGAGGAGTGAAGTGAAGTGAAGCTG 417
Qy 2272 AGATGGACCACTGCACT 2289
Db 418 AGATGGACCACTGCACT 435

RESULT 3
US-09-513-999C-395
; Sequence 395, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59. US2. REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 395

LENGTH: 344
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 54..344
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 54..119
OTHER INFORMATION: score 5.9
OTHER INFORMATION: seq LITLWQLTGSAA/SG
FEATURE:
NAME/KEY: misc_feature
LOCATION: 197
OTHER INFORMATION: k=g or c
US-09-513-999C-395

Query Match 12.3%; Score 331.6; DB 4; Length 344;
Best Local Similarity 99.7%; Pred. No. 1.9e-88;
Matches 331; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGTGGCTTCATTAGTGGCTGACCTTCAGAGACAAATATGGCTGTTCCCAACAT 60
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DB 193 AAGTTGACTTATTTGTGTGACCTTCAACACAAACCTCTTTGTCACTACAGCCAGAG 252
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DB 253 GGGGCACTATCATAGTGAACCAAAATGTATAGGGAGAGATGACTTCCCAATGAG 312
QY 301 GCTACTCCCTGAAGCTCAGCAAACTGAAGAAG 332
DB 313 GCTACTCCCTGAAGCTCAGCAAACTGAAGAAG 344

RESULT 4
US-09-705-299-13
Sequence 13, Application US/09705299
Patent No. 6440737
GENERAL INFORMATION:
APPLICANT: Lex M. Cowbert
APPLICANT: Susan M. Frieier
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR APOPTOSIS SUSCEPTIBILITY GENE
FILE REFERENCE: RTS-0174
CURRENT APPLICATION NUMBER: US/09/705,299
CURRENT FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 86
SEQ ID NO 13
LENGTH: 5037
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION:
NAME/KEY: unsure
LOCATION: 801
OTHER INFORMATION: unknown
US-09-705-299-13

Query Match 7.2%; Score 194.4; DB 4; Length 5037;
Best Local Similarity 79.9%; Pred. No. 7.6e-47;
Matches 254; Conservative 0; Mismatches 61; Indels 3; Gaps 2;

QY 2028 TTAAGAACCTACTATGCGGCGCCGAGTGGCTCAACCTGTATCCAGACCTTTGGG 2087
DB 2892 TTTAAAACTTAATCTTTGGTGGGCGGTGGGTCAACCTGTATCTAGACCTTTGGG 2951
QY 2088 AGGCCAAGTGGTGGTCACTTGAAGTCAAGAGTTCAAGACCAAGCCTGGCCAACTGGT 2147
DB 2952 AGGCCAAGTGGTGGTCACTTGAAGTCAAGAGTTCAAGAGCCTGGCCAACTGGC 3011
QY 2148 GAAACCCCTCTCTACTTAAAGATCAAAATTTGCTGAGCGTGGTGTGACCTGT-ATC 2206
DB 3012 GAAACCCCTCTCTACTTAAAGATCAAAATTTGCTGAGCGTGGTGTGACCTGTATC 3071
QY 2207 CCAGCTACTGAGAGCCCAAGCATGAGATCGCTTGAACCTGG--AGTGAAGTTGCAG 2264
DB 3072 CCAGCTACTGAGAGCCCAAGCATGAGATCGCTTGAACCTGGAGAGAGTTGGCAG 3131
QY 2265 TGAGCTGAGTGGACCACTGCACTCCGGCTTAGGCAAGAGCAAACTCCAATACAA 2324
DB 3132 TGAGCCAGATCCGCCATTTGCACTAGCTGGGCAACAAAGTGAATCCCTGTCA 3191
QY 2325 ACAACAAACAAACACT 2342
DB 3192 AGAAAAAAATTAATCTT 3209

RESULT 5
US-08-884-324-9
Sequence 9, Application US/08884324
Patent No. 6060283
GENERAL INFORMATION:
APPLICANT: Takemori OKURA
APPLICANT: Kakuji TORIOE
APPLICANT: Masahiro KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4773 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placenta
FEATURE:

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; NAME/KEY: intron
; LOCATION: 1..4773
; IDENTIFICATION METHOD: E
US-08-884-324-9

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Query Match	7.1%;	Score 190.8;	DB 3;	Length 4773;
Best Local Similarity	77.9%;	Pred. No. 8.6e-46;		
Matches 268; Conservative	0;	Mismatches 72;	Indels 4;	Gaps 3

OY	2004	GTTATATTCATTCAATAGATATTTATTTAAGAACTAATATGCGCGCCGGCATGCGGCTCA	2063
Db	1334	GTTATATCAATTTTGAATGGCCCTTTTAATATATTAAGAAATGTGGCTGGCGTGGTGCTCA	1393
OY	2064	CACCTGTATATCCACGACCTTTGGGAGGCGAAGTGGGTGCATCTAGGTCAGAGCTT	2123
Db	1394	CACCTGTATATCCACGACCTTTGGGAGGCGAAGGCGGAGTCACTTAAGTCAGAGATT	1453
OY	2124	CAAGACCAAGCTGGCCAAATGATGTAAGAAACCCCATCTCTAATAAAGT - CAAAATTTGCTG	2182
Db	1454	CAAGACCAAGCTGACCAATATGAGAAACCCCATCTCTAATAAATACAAAAATTAGCTG	1513
OY	2183	AGCGTGTGTGTGTGCACTGT - ATCCCAAGCTAATCTGAAGGCCAAAGGCAATGAAATGCT	2241
Db	1514	GGCGTGTGTGTGTGCAATATGCTGTATATCCAGCTAATCTGGAGGCTGAGGCGAGAGAAATCTTT	1573
OY	2242	TGAACCTGG - AGGTGAGGTGTCAGATGAGTGCAGATGCAACATGCACTCGGCGTAAAG	2299
Db	1574	TGAACCCGGGAGGCGAGAGGTGTTCAGATGAGCTTAAGTGTGCACTTGCACTCAAGCTGGG	1633
OY	2300	CAACGAGGCAAAATCTCCATATCAAAACAAACAAACAAACACTTG	2343
Db	1634	CAACGAGGCAAAATCTCGTCTCAAAAAAAAAAAAAAAAAAGTG	1677

RESULT 6
US-09-479-862-9

Sequence 9, Application US/09479862
Patent No. 6790442
GENERAL INFORMATION:
APPLICANT: TAKANOJI OKURA
APPLICANT: KAKUJI TORIGOE
APPLICANT: MASASHI KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
OF INDUCING THE PRODUCTION OF INTERFERON-
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,862

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? LENGTH: 4773 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: Genomic DNA
? ORIGINAL SOURCE:
? ORGANISM: human
? TISSUE TYPE: placenta
? FEATURE:
? NAME/KEY: intron
? LOCATION: 1..4773
? IDENTIFICATION METHOD: E
?
JS-09-479-862-9

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Query Match	7.1%;	Score 190.8;	DB 4;	Length 4773;
Best Local Similarity	77.9%;	Pred. No. 8.6e-46;		
Matches 268; Conservative	0;	Mismatches 72;	Indels 4;	Gaps 3

QY	2004	GTTAATTCATTCAATAGATATTATTAAAGAACTACTATGAGGCCCGGCATGTGCTCA	2065
Db	1334	GTATTATTCAAATTTTGAATGAGCCCTTTTAATATAAAAAGAAATGAGCTGGCGTGTGTGCTCA	1392
QY	2064	CACCTGTAAATCCAGCACTTTGGAGAGCCCAAGTGGGCTCATCTGAGTCAAGAT	2122
Db	1394	CACCTGTAAATCCAGCACTTTGGAGAGCCCAAGGGGGGGGATCACTGAATCAGAGATT	1455
QY	2124	CAAGACCAAGCTTGGCCCAACATGATGAAACCCCATCTCTACTAAAGAT-CAAAATTTGCTG	2188
Db	1454	CAAGACCAAGCTTGACCAACATGAGAAACCCCATCTCTACTAAAAATCAAAATTTAGCTG	1512
QY	2183	AGCGTGTGTTGTGCACTGT-ATCCACAGTACTTGAGAGGCCCAAGGCATAGAAATCGCT	2244
Db	1514	GGCGTGTGTCATATGCTCTGTAAATCCAGCTACTCGGAGAGCTGAGGCAGAGAAATCTTT	1572
QY	2242	TGAACCTTGG--AGGTGAGTTGGAGTAGCTGAAATGGCAACATGCACTCCGGCTAAG	2298
Db	1574	TGAACCCGGGAGGAGAGGTTGGCATGAGCTTAAGTCTGTGCATTGCACTCCAGCTTGGG	1632
QY	2300	CAAGGAGAGCAAAATCTCAATATACAAACAAACAAACACCTG	2343
Db	1634	CAACAGAGCAAAATCTGGTCTCAAAAAAAAAAAAAAAAAAGTG	1677

RESULT 7
US-08-88

Sequence 13, Application US/08864324
Patent No. 6060283
GENERAL INFORMATION:
APPLICANT: Takano,ri OKURA
APPLICANT: Kakuiji TORIGOE
APPLICANT: Maasaji KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 11464 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placenta
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..3
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 4..82
IDENTIFICATION METHOD: S
NAME/KEY: Intron
LOCATION: 83..1453
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 1454..1465
IDENTIFICATION METHOD: S
NAME/KEY: Intron
LOCATION: 1466..4848
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 4849..4865
IDENTIFICATION METHOD: S
NAME/KEY: mat peptide
LOCATION: 4866..4983
IDENTIFICATION METHOD: S
NAME/KEY: Intron
LOCATION: 4984..6317
IDENTIFICATION METHOD: E
NAME/KEY: mat peptide
LOCATION: 6318..6451
IDENTIFICATION METHOD: S
NAME/KEY: Intron
LOCATION: 6452..11224
IDENTIFICATION METHOD: E
NAME/KEY: mat peptide
LOCATION: 11225..11443
IDENTIFICATION METHOD: S
NAME/KEY: 3'UTR
LOCATION: 11444..11464
IDENTIFICATION METHOD: E
US-08-864-324-13

Query Match 7.1%; Score 190.8; DB 3; Length 11464;
Best Local Similarity 77.9%; Pred. No. 1.6e-45;
Matches 268; Conservative 0; Mismatches 72; Indels 4; Gaps 3;

QY 2004 GTTAATTCATTCATATAGATATTTATTAAGAACCTACTAGCGCCCGCGCATGGTGCTCA 2063
DB 7785 GTTATTAATTCATTTGATGAGCCCTTTTAATTAAGAAATGGTGCTGAGCGTGCTCA 7844
QY 2064 CACCTGTATTCACGACCTTTGGAGGCGCAAGTGGTGCTCATCTGAGGTCAGAGTT 2123
DB 7845 CACCTGTATTCACGACCTTTGGAGGCGCGAGGCGGATCACTGAGGTCAGAGTT 7904
QY 2124 CAAGACCAAGCTGGCGCAACATGATGAAACCCCATCTCTACTTAAGAT-CAAAATTTGCTG 2182
DB 7905 CAAGACCAAGCTGGCGCAACATGAGAAACCCCATCTCTACTTAAGATCAAAATTTAGCTG 7964
QY 2183 AGCGTGTGTGTGTACACTGT-ATCCAGAGTACTGAGAGGCGCAAGGATGAGATGCT 2241

DB 7965 GCGGTGGTGCATATGCTGTATATCCAGCTACTCGGAGGCTGAGGACAGAAATCTTT 8024
QY 2242 TGAACCTGG--AGTAGAGTTGTCAGTGAGCTGAGATGAGCACTGCACTCCGCGCTAGG 2299
DB 8025 TGAACCCGGAGGACAGAGGTTGGATGAGGCTGTGATCGTCATTCGACTCCAGCCTGGG 8084
QY 2300 CAAGAGAGCAAACTCCATACAAACAAAACAACACTG 2343
DB 8085 CAACAGAGCAAACTCGTCTCAAAAAAAAAAAAAAAAAAGTG 8128

RESULT 8
US-09-479-862-13
Sequence 13, Application US/09479862
Patent No. 6790442
GENERAL INFORMATION:
APPLICANT: Takano, OKURA
APPLICANT: Kakuji TORIOE
APPLICANT: Masahiro KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
NUMBER OF SEQUENCES: 35
OF INDUCING THE PRODUCTION OF INTERFERON-
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,862
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/864,324
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 11464 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placenta
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..3
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 4..82
IDENTIFICATION METHOD: S
NAME/KEY: Intron
LOCATION: 83..1453
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 1454..1465
IDENTIFICATION METHOD: S
NAME/KEY: Intron

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1 LOCATION: 1466..4848
2 IDENTIFICATION METHOD: E
3 NAME/KEY: leader peptide
4 LOCATION: 4849..4865
5 IDENTIFICATION METHOD: S
6 NAME/KEY: mat peptide
7 LOCATION: 4866..4983
8 IDENTIFICATION METHOD: S
9 NAME/KEY: inton
10 LOCATION: 4984..6317
11 IDENTIFICATION METHOD: E
12 NAME/KEY: mat peptide
13 LOCATION: 6318..6451
14 IDENTIFICATION METHOD: S
15 NAME/KEY: inton
16 LOCATION: 6452..11224
17 IDENTIFICATION METHOD: E
18 NAME/KEY: mat peptide
19 LOCATION: 11225..11443
20 IDENTIFICATION METHOD: S
21 NAME/KEY: 3'UTR
22 LOCATION: 11444..11664
23 IDENTIFICATION METHOD: E

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Query Match	7.1%;	Score 190.8;	DB 4;	Length 1146;
Best Local Similarity	77.9%;	Pred. NO. 1.6e-45;		
Matches 268; Conservative	0;	Mismatches 72;	Indels 4;	Gaps 3;

Qy	2004	GTAAATTCATTCATAGATATTTATTAAGACCTCTATGAGGCCCGGCATGTGGCTCA	2063
Db	7785	GTTATATCAATTTTGATGGCCCTTTTAATATTAAGAATGTGGCGGTGGTGCTCA	7844
Qy	2064	CACCTGTATATCCAGACACTTTGGGAGGCGCAAGGTGGGTCACTTAAGTCAGAGATT	2123
Db	7845	CACCTGTATATCCAGACACTTTTGGAGGCGGAGGGGGGATATCATCTTAAGTCAGAGATT	7904
Qy	2124	CAAGACCAAGCTGAGCACAATGATGTGAAGAACCCCATCTCTACTTAAGAT-CAAAATTTGCTG	2182
Db	7905	CAAGACCAAGCTGAGCACAATGAGAAACCCCATCTCTACTTAAGATCAAAAATTAAGCTG	7964
Qy	2183	AGCTGTGTGTGTGCACCTGT-ATTCACAGCTACTGAGAGGCGCAAGGCATGGAATGCT	2241
Db	7965	GGCCTGTGTGTGTATGTCTGTATATCCAGCTACTGCGGAGGCTGAGGACAGAGAACTTT	8024
Qy	2242	TGAACCTGG-AGGTGAGGTGCAATGAGTGCAGTGCACCACTGCCTCGGCTAGG	2299
Db	8025	TGAACCGGAGGAGCAGAGGTGGCATGAGCTTAAGTGTGCTCATTTGCACCTCAGCGCTGG	8084
Qy	2300	CAACGAGAGCAAAATCTCCATATCAAAACAACAAACACCTG	2343
Db	8085	CAACGAGAGCAAAATCTCGGTCTCAAAAAAAAAAAAAAAAAAGTG	8128

RESULT 9
 US-08-884-324-14
 : Sequence 14, Application US/08884324
 : Patent No. 6060283
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: TAKANO, I. OKURA
 : APPLICANT: KAKUJI TORIGOE
 : APPLICANT: MASASHI KURIMOTO
 : TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
 : OF INDUCING THE PRODUCTION OF INTERFERON-
 :
 : NUMBER OF SEQUENCES: 35
 :
 : CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:

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1  MEDIAN TYPE: floppy disk
2  COMPUTER: IBM PC compatible
3  OPERATING SYSTEM: PC-DOS/MS-DOS
4  SOFTWARE: Patent in Release #1.0, Version #1.30
5  CURRENT APPLICATION DATA:
6  APPLICATION NUMBER: US/08/884,324
7  FILING DATE:
8  CLASSIFICATION: 435
9  PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: JP 185,305/96
11 FILING DATE: 27-JUN-1996
12 ATTORNEY/AGENT INFORMATION:
13 NAME: BROWDY, Roger L.
14 REGISTRATION NUMBER: 25,618
15 REFERENCE/DOCKET NUMBER: OKURA=1
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: 202-628-5197
18 TELEFAX: 202-737-3528
19 INFORMATION FOR SEQ ID NO: 14:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 28994 base pairs
22 TYPE: nucleic acid
23 STRANDEDNESS: double
24 TOPOLOGY: linear
25 MOLECULE TYPE: Genomic DNA
26 ORIGINAL SOURCE:
27 ORGANISM: human
28 TISSUE TYPE: placenta
29 FEATURE:
30 NAME/KEY: 5'UTR
31 LOCATION: 1..15606
32 IDENTIFICATION METHOD: E
33 NAME/KEY: leader peptide
34 LOCATION: 15607..15685
35 IDENTIFICATION METHOD: S
36 NAME/KEY: intron
37 LOCATION: 15686..17056
38 IDENTIFICATION METHOD: E
39 NAME/KEY: leader peptide
40 LOCATION: 17057..17068
41 IDENTIFICATION METHOD: S
42 NAME/KEY: intron
43 LOCATION: 17069..20451
44 IDENTIFICATION METHOD: E
45 NAME/KEY: leader peptide
46 LOCATION: 20452..20468
47 IDENTIFICATION METHOD: S
48 NAME/KEY: mat peptide
49 LOCATION: 20469..20586
50 IDENTIFICATION METHOD: S
51 NAME/KEY: intron
52 LOCATION: 20587..21920
53 IDENTIFICATION METHOD: E
54 NAME/KEY: mat peptide
55 LOCATION: 21921..22054
56 IDENTIFICATION METHOD: S
57 NAME/KEY: intron
58 LOCATION: 22055..26827
59 IDENTIFICATION METHOD: E
60 NAME/KEY: mat peptide
61 LOCATION: 26828..27046
62 IDENTIFICATION METHOD: S
63 NAME/KEY: 3'UTR
64 LOCATION: 27047..28994
65 IDENTIFICATION METHOD: E
66
67 US-08-884-324-14
68
69 Query Match 7.1%; Score 190.8; DB 3; Length 28994;
70 Best Local Similarity 77.9%; Pred. No. 2,9e-45;
71 Matches 266; Conservative 0; Mismatches 72; Indels 4; Gaps 3
72
73 2004 GTTAAATTCATTCATAGATATTTATTAAGAACTACTATATGCGGCCGCGCATGTGTGCTCA 2063

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Db 23388 GTTATTCATTTGATGACCTTTTAAATATAAAGATGTGGCGTGTGCTCA 23447
 QY 2064 CACCTGTAATCCAGCACTTTGGAGCCAAAGTGGGTGCTATCTGAGTCAAGAGTT 2123
 Db 23448 CACCTGTAATCCAGCACTTTGGAGCCAAAGTGGGTGCTATCTGAGTCAAGAGTT 23507
 QY 2124 CAAGACCAAGCTGGCCAAATGAGTGAACCCCACTCTCTAATAAGAT-CAAAATTTGCTG 2182
 Db 23508 CAAGACCAAGCTGGCCAAATGAGTGAACCCCACTCTCTAATAAGAT-CAAAATTTGCTG 23567
 QY 2183 AGCGTGTGTGTGACCTGT-ATCCAGCTACTCGAGAGCCAAAGCATGAGATGCT 2241
 Db 23568 GCGTGTGTGCAATGCTGTATCCAGCTACTCGAGAGCCAAAGCATGAGATGCT 23627
 QY 2242 TGAACCTGG--AGTGAAGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2239
 Db 23628 TGAACCTGGAGGAGGAGGAGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 23687
 QY 2300 CAACGAGAGCAAACTCCATATACAAACAAACAAACAAACCTG 2343
 Db 23688 CAACGAGAGCAAACTCCATATACAAACAAACAAACAAACCTG 23731
 RESULT 10
 US-09-479-862-14
 ; Sequence 14, Application US/09479862
 ; Patent No. 6790442
 ; GENERAL INFORMATION:
 ; APPLICANT: Takamori OKURA
 ; APPLICANT: Kakuji TORIGOE
 ; APPLICANT: Masahito KURIMOTO
 ; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
 ; OF INDUCING THE PRODUCTION OF INTERFERON-
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROMDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; City: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/479,862
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/884,324
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROMDY, Roger L.
 ; REGISTRATION NUMBER: OKURA=1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 28994 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Genomic DNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: human
 ; TISSUE TYPE: placenta
 ; FEATURE:
 ; NAME/KEY: 5'UTR
 ; LOCATION: 1..15606

; IDENTIFICATION METHOD: E
 ; NAME/KEY: leader peptide
 ; LOCATION: 15607..15685
 ; IDENTIFICATION METHOD: S
 ; NAME/KEY: intron
 ; LOCATION: 15686..17056
 ; IDENTIFICATION METHOD: B
 ; NAME/KEY: leader peptide
 ; LOCATION: 17057..17068
 ; IDENTIFICATION METHOD: S
 ; NAME/KEY: intron
 ; LOCATION: 17069..20451
 ; IDENTIFICATION METHOD: B
 ; NAME/KEY: leader peptide
 ; LOCATION: 20452..20468
 ; IDENTIFICATION METHOD: S
 ; NAME/KEY: mat peptide
 ; LOCATION: 20469..20586
 ; IDENTIFICATION METHOD: S
 ; NAME/KEY: intron
 ; LOCATION: 20587..21920
 ; IDENTIFICATION METHOD: E
 ; NAME/KEY: mat peptide
 ; LOCATION: 21921..22054
 ; IDENTIFICATION METHOD: S
 ; NAME/KEY: intron
 ; LOCATION: 22055..26827
 ; IDENTIFICATION METHOD: E
 ; NAME/KEY: mat peptide
 ; LOCATION: 26828..27046
 ; IDENTIFICATION METHOD: S
 ; NAME/KEY: 3'UTR
 ; LOCATION: 27047..28994
 ; IDENTIFICATION METHOD: E
 ; US-09-479-862-14
 Query Match 7.1%; Score 190.8; DB 4; Length 28994;
 Best Local Similarity 77.9%; Pred. No. 2.9e-45;
 Matches 268; Conservative 0; Mismatches 72; Indels 4; Gaps 3;
 QY 2004 GTTATTCATTCATGATATTTATTAAGAACTTATGAGCCCGGATGCTGCTCA 2063
 Db 23388 GTTATTCATTTGATGACCTTTTAAATATAAAGATGTGGCGTGTGCTCA 23447
 QY 2064 CACCTGTAATCCAGCACTTTGGAGCCAAAGTGGGTGCTATCTGAGTCAAGAGTT 2123
 Db 23448 CACCTGTAATCCAGCACTTTGGAGCCAAAGTGGGTGCTATCTGAGTCAAGAGTT 23507
 QY 2124 CAAGACCAAGCTGGCCAAATGAGTGAACCCCACTCTCTAATAAGAT-CAAAATTTGCTG 2182
 Db 23508 CAAGACCAAGCTGGCCAAATGAGTGAACCCCACTCTCTAATAAGAT-CAAAATTTGCTG 23567
 QY 2183 AGCGTGTGTGTGACCTGT-ATCCAGCTACTCGAGAGCCAAAGCATGAGATGCT 2241
 Db 23568 GCGTGTGTGCAATGCTGTATCCAGCTACTCGAGAGCCAAAGCATGAGATGCT 23627
 QY 2242 TGAACCTGG--AGTGAAGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2239
 Db 23628 TGAACCTGGAGGAGGAGGAGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 23687
 QY 2300 CAACGAGAGCAAACTCCATATACAAACAAACAAACAAACCTG 2343
 Db 23688 CAACGAGAGCAAACTCCATATACAAACAAACAAACAAACCTG 23731
 RESULT 11
 US-10-148-806-3
 ; Sequence 3, Application US/10148806
 ; Patent No. 6762042
 ; GENERAL INFORMATION:
 ; APPLICANT: Bai, Chang
 ; APPLICANT: Metzger, Michael
 ; APPLICANT: Liu, Xiaomei

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/ TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
/ FILE OF INVENTION: HELICASE
/ FILE REFERENCE: 20585P
/ CURRENT APPLICATION NUMBER: US/10/148,806
/ PRIOR FILING DATE: 2002-06-05
/ PRIOR APPLICATION NUMBER: US00/33065
/ PRIOR FILING DATE: 2000-12-09
/ PRIOR APPLICATION NUMBER: 60/169,970
/ PRIOR FILING DATE: 1999-12-09
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 114793
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-148-806-3

Query Match      7.0%; Score 189.4; DB 4; Length 114793;
Best Local Similarity 77.8%; Pred. No. 1.9e-44;
Matches 267; Conservative 0; Mismatches 71; Indels 5; Gaps 3;

QY 2007 AATTCATTCATATGATATTTATTAAGACCTATGCGCCCGCATGTGGCTCACAC 2066
DB 106789 ACTGCACCTTAATTAATTTCTTTTATATAGTTTTCAGAGGCCAGCAGCTGCTCACAC 106848
QY 2067 CTGTAAATCCAGACACTTTTGAGGAGCCAGAGTGGGTCTATCTGAGTCCAGAGTTCAA 2126
DB 106849 CTGTATATCCAGACACTTTTGAGGAGCCAGAGTGGGTGATCACCCTAAGTCCAGAGTTGCA 106908
QY 2127 GACCAAGCTGGCCCAATAGTGTAAACCCCATCTCTAATAAGAT--CAAAATTTGCTGAG 2184
DB 106909 GACCAAGCTGGCCCAATAGTGTAAACCCCATCTCTAATAAGATCAAAATTAAGCTGGG 106968
QY 2185 CGTGGTGTGTGACCTGT-ATCCAGCTACTCGAAGAGCCAAAGGATGAGATGCTGG 2243
DB 106969 CGTGGTGTGTGACCTGT-ATCCAGCTACTCGAAGAGCTGAGAGGCTGAGGAGAGATCGCTGG 107028
QY 2244 AACCTGG--AGGTGAGGTTCAGATGAGCTGAGATGCGACACTGCACTCCGCTTAGGCA 2301
DB 107029 AACCTGGAGGAGGAGAGTGGTTCAGATGAGCCAGGATCAACACATTTGCACTCCAGCTGGTGA 107088
QY 2302 AGCAGAGCAAACTCCATATACAAACAAACAAACAAACCTGT 2344
DB 107089 ACMAAGCAAACTCCATCTCAAGAAAGAAAAAAGTTT 107131

RESULT 12
US-09-820-924-3
/ Sequence 3, Application US/09820924
/ Patent No. 655351
/ GENERAL INFORMATION:
/ APPLICANT: BEASLEY, Ellen M. et al
/ TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
/ FILE REFERENCE: CL001213
/ CURRENT APPLICATION NUMBER: US/09/820,924
/ CURRENT FILING DATE: 2001-03-30
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 39982
/ TYPE: DNA
/ ORGANISM: Human
US-09-820-924-3

Query Match      7.0%; Score 188.4; DB 4; Length 39982;
Best Local Similarity 80.8%; Pred. No. 1.9e-44;
Matches 257; Conservative 0; Mismatches 56; Indels 5; Gaps 3;

QY 2027 ATTAAGAACTACTATGCGCGCGGAGATGCTGCTACACCTGTATATCCAGACACTTTGG 2086
DB 19834 AATATTATTAAGAAATGAGGCGAGTGTGTCTCACCCTGTATATCCAGACACTTTGG 19893
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QY 2087 GAGCCAAAGTGGGTGCTATCTGAGGTCAAGATTCAAGACCGACCTGGCCAAATGG 2146
DB 19894 GAAGCTGAGTGGGTGGATCACTGTAAGTCAAGAAATCAAGACCGACCTGGCCAAATGG 19953
QY 2147 TGAACCCCATCTCTACTAAAGAT--CAAAATTTGCTAGAGGTGTGTGCACTGT- 2203
DB 19954 TGAACCCCATCTCTACTAAAGAT--CAAAATTTGCTAGAGGTGTGTGCTGCACTGT 20013
QY 2204 ATCCAGCTACTCGAGAGCCAAAGGATGAGAAATGCTTGAACCTGG--AGGTGAGTTG 2261
DB 20014 ATCCAGCTACTCGAGAGCTTAAGGAGAGAAATGCTTGAACCTGGAGGAGGAGTTG 20073
QY 2262 CAGTGAAGTGAATGAGCAGCACTGCACTCCGCTTAGGCAAGAGCAAAATCTCAATA 2321
DB 20074 TAGTGAAGCAGAGATCAACCAATTTGCACTCCAGCTGGCAATTAAGAGTGAATTCATCT 20133
QY 2322 CAACCAAAACAACAACA 2339
DB 20134 CAACCAAAACAACAACA 20151

RESULT 13
US-10-369-626-3
/ Sequence 3, Application US/10369626
/ Patent No. 6787344
/ GENERAL INFORMATION:
/ APPLICANT: BEASLEY, Ellen M. et al
/ TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
/ FILE REFERENCE: CL001213DIV
/ CURRENT APPLICATION NUMBER: US/10/369,626
/ CURRENT FILING DATE: 2003-02-21
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 39982
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-369-626-3

Query Match      7.0%; Score 188.4; DB 4; Length 39982;
Best Local Similarity 80.8%; Pred. No. 1.9e-44;
Matches 257; Conservative 0; Mismatches 56; Indels 5; Gaps 3;

QY 2027 ATTAAGAACTACTATGCGCGCGGAGATGCTGCTACACCTGTATATCCAGACACTTTGG 2086
DB 19834 AATATTATTAAGAAATGAGGCGAGGCTGTGTCTCACCCTGTATATCCAGACACTTTGG 19893
QY 2087 GAGCCAAAGTGGGTGCTATCTGAGGTCAAGATTCAAGACCGACCTGGCCAAATGG 2146
DB 19894 GAAGCTGAGTGGGTGGATCACTGTAAGTCAAGAAATCAAGACCGACCTGGCCAAATGG 19953
QY 2147 TGAACCCCATCTCTACTAAAGAT--CAAAATTTGCTAGAGGTGTGTGCACTGT- 2203
DB 19954 TGAACCCCATCTCTACTAAAGAT--CAAAATTTGCTAGAGGTGTGTGCTGCACTGT 20013
QY 2204 ATCCAGCTACTCGAGAGCCAAAGGATGAGAAATGCTTGAACCTGG--AGGTGAGTTG 2261
DB 20014 ATCCAGCTACTCGAGAGCTTAAGGAGAGAAATGCTTGAACCTGGAGGAGGAGTTG 20073
QY 2262 CAGTGAAGTGAATGAGCAGCACTGCACTCCGCTTAGGCAAGAGCAAAATCTCAATA 2321
DB 20074 TAGTGAAGCAGAGATCAACCAATTTGCACTCCAGCTGGCAATTAAGAGTGAATTCATCT 20133
QY 2322 CAACCAAAACAACAACA 2339
DB 20134 CAACCAAAACAACAACA 20151

RESULT 14
US-09-345-882-1/c
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Sequence 1, Application US/09345882
Patent No. 6399373
GENERAL INFORMATION:
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBB-7)
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIORITY APPLICATION NUMBER: US 60/091,315
PRIORITY FILING DATE: 1998-06-30
PRIORITY APPLICATION NUMBER: US 60/111,509
PRIORITY FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 162450
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 72794
OTHER INFORMATION: 5-124-273 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 90842
OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 93714
OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
FEATURE:
NAME/KEY: allele
LOCATION: 97122
OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
FEATURE:
NAME/KEY: allele
LOCATION: 99098
OTHER INFORMATION: 5-130-257 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 99117
OTHER INFORMATION: 5-130-276 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
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NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE:
NAME/KEY: allele

LOCATION: 108471
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
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OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE:
NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
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NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
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LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
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NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
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NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
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OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177

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/ OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID3
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 97130..97177
/ OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 99075..99121
/ OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 99075..99121
/ OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 99094..99140
/ OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 99094..99140
/ OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 103783..103828
/ OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 103783..103828
/ OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 106918..106966
/ OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 106918..106966
/ OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 108084..108130
/ OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 108084..108130
/ OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 108127..108177
/ OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 108127..108177
/ OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 108127..108177
/ OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID50

Query Match      6.9%; Score 187.4; DB 3; Length 162450;
Best Local Similarity 78.3%; Pred. No. 9.6e-44;
Matches 275; Conservative 0; Mismatches 71; Indels 5; Gaps 4;

QY 2028 TTAAGAACTACTATGCGCGCCGCGCATGTGGCTCAACCTGTAATCCAGACATTGGG 2087
DB 133068 TTAAGAACTACTATGCGCGCGCATGTGGCTCAACCTGTAATCCAGACATTGGG 133009
QY 2088 AGGCAAGGTGGGTGGTGCATGAGGTGAGAGTTCAAGACAGCGTGGCAACATGGT 2147
DB 133008 AGGCAAGGTGGGTGGTGCATGAGGTGAGAGTTCAAGACAGCGTGGCAACATGGT 132949
QY 2148 GAAACCCCATCTCTAATAAGAT--CAAAATTGCTGACCGTGTGTGTGACCTGT-A 2204
DB 132948 GAAACCCCATCTCTAATAAGAT--CAAAATTGCTGACCGTGTGTGTGACCTGT-A 132889
QY 2205 TCCGAGCTACTGAGAGGCGCAAGGATGGAATCGCTTGAACCTGGAGGT-GAGTTGCA 2263
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DB 132888 TCCGAGCTACTGAGAGGCGTGAAGCATGGAATCGCTTGAACCTGGAGGTGAGTTGCA 132829
QY 2264 GTGAGCTGAGATGGCACCCTGACTCCGCTAGGACAAGCAAACTCCAATACA 2323
DB 132828 GTGAGCTGAGATGGCACCCTGACTCCGCTAGGACAAGCAAACTCCAATACA 132770
QY 2324 AAGAACCAACCAACACCTGTGTGCTAGTCAAGTCTGGCAGTGAATGAACA 2374
DB 132769 AAAAAAAAAAAAAATCTTGTAATATATCTTAAGCCACTGACTATATCA 132719

RESULT 15
US-09-539-333D-1
/ Sequence 1, Application US/09539333D
/ Patent No. 6476208
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Daniel
/ APPLICANT: Blumenfeld, Marta
/ APPLICANT: Chumakov, Ilya
/ APPLICANT: Bougueleret, Lydie
/ APPLICANT: Bihain, Bernard
/ APPLICANT: Essioux, Laurent
/ TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
/ FILE REFERENCE: GENSET.047AUS
/ CURRENT APPLICATION NUMBER: US/09/539, 333D
/ PRIOR FILING DATE: 2000-03-30
/ PRIOR APPLICATION NUMBER: US 60/126,903
/ PRIOR FILING DATE: 1999-03-30
/ PRIOR APPLICATION NUMBER: US 60/131,971
/ PRIOR FILING DATE: 1999-04-30
/ PRIOR APPLICATION NUMBER: US 60/132,065
/ PRIOR FILING DATE: 1999-04-30
/ PRIOR APPLICATION NUMBER: US 60/143,928
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: US 60/145,915
/ PRIOR FILING DATE: 1999-07-27
/ PRIOR APPLICATION NUMBER: US 60/146,453
/ PRIOR FILING DATE: 1999-07-29
/ PRIOR APPLICATION NUMBER: US 60/146,452
/ PRIOR FILING DATE: 1999-07-29
/ PRIOR APPLICATION NUMBER: US 60/162,288
/ PRIOR FILING DATE: 1999-10-28
/ PRIOR APPLICATION NUMBER: US 09/416,384
/ PRIOR FILING DATE: 1999-10-12
/ NUMBER OF SEQ ID NOS: 231
/ SOFTWARE: Patent.pm
/ SEQ ID NO 1
/ LENGTH: 319608
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 31..1107
/ OTHER INFORMATION: 5' regulatory region g35018 gene
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 1108..1289
/ OTHER INFORMATION: exon A g35018 gene
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 14877..14920
/ OTHER INFORMATION: exon B g35018 gene
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 18778..18862
/ OTHER INFORMATION: exon Bbis g35018 gene
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/ NAME/KEY: exon
/ LOCATION: 25593..25740
/ OTHER INFORMATION: exon C g35018 gene
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 29386..29502
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OTHER INFORMATION: exon F g35018 gene
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LOCATION: 65505..65853
OTHER INFORMATION: exon G g35018 gene
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NAME/KEY: misc feature
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OTHER INFORMATION: 3'regulatory region g35018 gene
FEATURE:
NAME/KEY: exon
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OTHER INFORMATION: exon g35017
FEATURE:
NAME/KEY: exon
LOCATION: 201188..201234
OTHER INFORMATION: exon S g35030 gene
FEATURE:
NAME/KEY: exon
LOCATION: 214676..214793
OTHER INFORMATION: exon T g35030 gene
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NAME/KEY: exon
LOCATION: 216836..216915
OTHER INFORMATION: exon V g35030 gene
FEATURE:
NAME/KEY: misc feature
LOCATION: 215818..215818
OTHER INFORMATION: 3'regulatory region g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 215819..215941
OTHER INFORMATION: exon R complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 215819..215975
OTHER INFORMATION: exon Rbis complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 216661..216952
OTHER INFORMATION: exon Qbis complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 216661..217061
OTHER INFORMATION: exon Q complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 217027..217061
OTHER INFORMATION: exon Q1 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 229647..229742
OTHER INFORMATION: exon X complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 230408..230721
OTHER INFORMATION: exon P complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 231272..231412
OTHER INFORMATION: exon Obis complement g34872 gene

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NAME/KEY: exon
LOCATION: 231787..231880
OTHER INFORMATION: exon O2 complement g34872 gene
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OTHER INFORMATION: exon M117 complement g34872 gene
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OTHER INFORMATION: exon M1069 complement g34872 gene
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OTHER INFORMATION: exon M862 complement g34872 gene
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OTHER INFORMATION: exon M692 complement g34872 gene
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NAME/KEY: exon
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OTHER INFORMATION: exon M1 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240800..240993
OTHER INFORMATION: exon M51 complement g34872 gene
FEATURE:
NAME/KEY: misc feature
LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory region g34872 gene
FEATURE:
NAME/KEY: misc feature
LOCATION: 290652..292652
OTHER INFORMATION: 3'regulatory region g34665 gene
FEATURE:
NAME/KEY: exon
LOCATION: 292653..292841

Query Match 6.9%; Score 187.4; DB 4; Length 319608;
Best Local Similarity 81.7%; Pred. No. 1.5e-43;
Matches 254; Conservative 0; Mismatches 51; Indels 6; Gaps 3;
OY 2036 CTACTATGGCGGCCCGCATGTGCTCACACCTGTAAATCCAGCACTTTGGAGGCCAAG 2095

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Db      88344 CTTAAAGGGGCGGGGTATGCTCACACCTGTAATCCAGCACTTTGGGAGGCCGAG 88403
QY      2096 GTGGGTGGGTCATCTGAGGTCAAGGATGAAGCCAGCCTGGCCCAATGGTGAACCCC 2155
Db      88404 GTGGGTGAATCACCTGAGATCAGAAATTCAAGACAGCCTGGCTAATAGTGAACCCA 88463
QY      2156 ATCTCTACTTAAGAT--CAAAATTTGCTGAGCGGTGGGTGTGCACTGT-ATCCGAGC 2211
Db      88464 GTCTTACTTAAATAACAAAAAATAGCAGGCGCATGTGGCGGCTGCTGTATCCGAGC 88523
QY      2212 TACTCGAGAGGCCAAGGCATGAGATCGCTTGAACCTGG--AGGTGAGTTGCAGTGAGC 2269
Db      88524 TGCTCGGAGGCTGAGGCAAGAAATTGCTTGAACCTGGGAAAGCAGAGGTTGCAGTGAGC 88583
QY      2270 TGAGATGCGACCACTGCACTCGGCGCTAGGCAACGAGCAAACTCCAAATCAAAACAA 2329
Db      88584 TGAGGTCAAGCCATTGCACTCCAGCTGGGCAACAAAGATGAATTCATCACACACACA 88643
QY      2330 CAAACAAACAC 2340
Db      88644 CACACACACAC 88654
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Search completed: October 28, 2004, 10:20:41
Job time : 228 secs

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C	94	63	2,3	152224	9	AC144536	Homo sapi
C	95	63	2,3	152354	2	AC016472	Homo sapi
C	96	63	2,3	152582	2	AC027014	Homo sapi
C	97	63	2,3	153356	2	AC004995	Homo sapi
C	98	63	2,3	153471	2	AC027076	Homo sapi
C	99	63	2,3	155085	9	AC010412	Homo sapi
C	100	63	2,3	155313	2	AC068315	Homo sapi

ALIGNMENTS

RESULT 1	AXI80364	2704 bp	DNA	linear	PAT 06-AUG-2001
LOCUS	AXI80364	Sequence 1 from Patent WO0146260.			
DEFINITION	AXI80364				
ACCESSION	AXI80364				
VERSION	AXI80364.1	GI:15132304			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE
AUTHORS
TITLE
1 Starling, G.C. and Finger, J.
Novel immunoglobulin superfamily members apex-1, apex-2 and apex-3
and uses thereof
Patent: WO 0146260-A 1 28-JUN-2001;
Bristol-Myers Squibb Co. (US)
Location/Qualifiers
1. .2704

FEATURES
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ORIGIN

Query Match 100.0%; Score 2704; DB 6; Length 2704;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2704; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGAGGCGCTTCATTTTCAGTGGCTGACTTCAGAGCAATATGGCTGTCCCAACAT	60
DB	1	GGAGGCGCTTCATTTTCAGTGGCTGACTTCAGAGCAATATGGCTGTCCCAACAT	60
QY	61	GCCTCACCCCTCATCTATCTTTGGAGCTCAAGGTCAGAGCCTCGAACCCTGA	120
DB	61	GCCTCACCCCTCATCTATCTTTGGAGCTCAAGGTCAGAGCCTCGAACCCTGA	120
QY	121	AAGAGCTGTGCGGTTCGTTGATGGGCGCTGACTTTCCCTGAAGTCCAAAGTAAG	180
DB	121	AAGAGCTGTGCGGTTCGTTGATGGGCGCTGACTTTCCCTGAAGTCCAAAGTAAG	180
QY	181	AAATTGACTTATTTGCTGGAAGCTTCAACAACCCCTCTTTCACCATACAGCCGAAG	240
DB	181	AAATTGACTTATTTGCTGGAAGCTTCAACAACCCCTCTTTCACCATACAGCCGAAG	240
QY	241	GGGGAAGTATCATAGTGAACCAAAATCGTAATAGGGAGAGTGAAGTCCCGATGGAG	300
DB	241	GGGGAAGTATCATAGTGAACCAAAATCGTAATAGGGAGAGTGAAGTCCCGATGGAG	300
QY	301	GCTACTCCCTGAAGCTCAGCAAACTGAGAAAGATGCTCAGGATCTATATGGGGA	360
DB	301	GCTACTCCCTGAAGCTCAGCAAACTGAGAAAGATGCTCAGGATCTATATGGGGA	360
QY	361	TATACAGCTCATCATCTCCAGAGCCTCCACCAAGAGTACGCTGCATGTCTACAGC	420
DB	361	TATACAGCTCATCATCTCCAGAGCCTCCACCAAGAGTACGCTGCATGTCTACAGC	420
QY	421	ACCTGCAAGGCTTAAGTCAACATGGGCTGAGAGCAATTAAGATGGACCTGTGTGA	480
DB	421	ACCTGCAAGGCTTAAGTCAACATGGGCTGAGAGCAATTAAGATGGACCTGTGTGA	480

QY	481	CCAATTCGACATGCTGATGAAACATGAGGAAAGATGTGATTTATACCTGGAAAGCCC	540
DB	481	CCAATTCGACATGCTGATGAAACATGAGGAAAGATGTGATTTATACCTGGAAAGCCC	540
QY	541	TGGGGAAGCAGCAGCAATGATGCTCATATGGGTCATCTCCCATCTCTGGAGATGGG	600
DB	541	TGGGGAAGCAGCAGCAATGATGCTCATATGGGTCATCTCCCATCTCTGGAGATGGG	600
QY	601	GAGAAAGTATGATGACCTTCATCTGCTGAGGAGCAAGCCTGTCAGAGAACTTCTCA	660
DB	601	GAGAAAGTATGATGACCTTCATCTGCTGAGGAGCAAGCCTGTCAGAGAACTTCTCA	660
QY	661	GCCCCATCTTGGCAGAGAGCTCTGAGAGGTGCTGATGATCCAGATTCCTCATGG	720
DB	661	GCCCCATCTTGGCAGAGAGCTCTGAGAGGTGCTGATGATCCAGATTCCTCATGG	720
QY	721	TCTCTCTGTGTCTCTGTGTGTGCTGCTCTGCTCATGTTCTTTGTACTGGGCTATTTTC	780
DB	721	TCTCTCTGTGTCTCTGTGTGTGCTGCTCTGCTCATGTTCTTTGTACTGGGCTATTTTC	780
QY	781	TTTGTGTTTCTGAAGAGAGAGAGCAAGAGATGATGAGAGAGAGAGAGAGAGAGAG	840
DB	781	TTTGTGTTTCTGAAGAGAGAGAGCAAGAGATGATGAGAGAGAGAGAGAGAGAGAG	840
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DB	841	TTTGTGAGAACTCTTAACATATAGCCCCCATTTCTGAGAGAGACAGAGTACAGACAA	900
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DB	901	TCCCTCACCTAATGAGCAATCTTAAGAGAGATTCAGCAATTCGTTTACTCATCTG	960
QY	961	TGGAATATCCGAAAG	1020
DB	961	TGGAATATCCGAAAG	1020
QY	1021	GCGTATTTGCTATGAGAGATGTTATCTAGACAGAGTGCATCCCTAAGTCTGTCTCA	1080
DB	1021	GCGTATTTGCTATGAGAGATGTTATCTAGACAGAGTGCATCCCTAAGTCTGTCTCA	1080
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DB	1081	AAAAAAACAAATTTCTCGGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1140
QY	1141	AACATCAAG	1200
DB	1141	AACATCAAG	1200
QY	1201	CTTGAATTTAAGAGTTCGTAATTCATTCACCTGCTGAGAGAGAGAGAGAGAGAG	1260
DB	1201	CTTGAATTTAAGAGTTCGTAATTCATTCACCTGCTGAGAGAGAGAGAGAGAGAG	1260
QY	1261	GTTTATACCTTCATTCCTCAAAATGGAGTTGGAATGTCAGAAACCATTAAGAGAG	1320
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QY	1381	TATTAATGATGCTCAGGTGATGCTGAGAGTTTCATTCATCCAGAGGCTTGATGTC	1440
DB	1381	TATTAATGATGCTCAGGTGATGCTGAGAGTTTCATTCATCCAGAGGCTTGATGTC	1440
QY	1441	AGGATTTATCCAAAGTCTTGTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1500
DB	1441	AGGATTTATCCAAAGTCTTGTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1500
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Qy      1861 GTTTTAAGGCTGTCAGAAACCATCCCAATTAAGAGACCGAGTCTGAAGTCAATTTGA 1920
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Db      2161 TACTAAAGATCAAAATTTGCTGAGCGTGTGTGTGTCACCTGTATCCCACTACTCGAGA 2220
Qy      2221 GGGCAAGGCAATGAAATCGCTTGAACCTGGAAGGAGTGTGAGTGTGAGATGCGAC 2280
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Qy      2281 CACTGCACTCCGGCTTAGGCAAGAGCAAACTCCAATATCAAAACAAACAAACAC 2340
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Qy      2461 TCCCTGACGATATCTTGAATGAGACCTCCCTACCAAGTGAAGATGTTGAAAAACT 2520
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Qy      2581 TTGTGAAGGAATGAGCAAGATCTCTCTCTACTGAAATCCCTATTTGATGAAGAAAG 2640
Db      2581 TTGTGAAGGAATGAGCAAGATCTCTCTCTACTGAAATCCCTATTTGATGAAGAAAG 2640
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Db      2641 TCTTCTTACTATCTTATATAAAGATATTTGTGAGATTCAATTAATTAATTAAT 2700
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RESULT 2
AB027233
LOCUS      2672 bp. mRNA linear PRI 21-JUN-2001
DEFINITION Homo sapiens mRNA for membrane protein FOAP-12, complete cds.
ACCESSION AB027233
VERSION    AB027233.1 GI:14517605
KEYWORDS   membrane protein FOAP-12.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1 (bases 1 to 2672)
            Fujii,Y., Takayama,K., Tsuritani,K., Yajima,Y., Amemiya,T.,
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            Homo sapiens mRNA for FOAP-12 protein, complete cds
            Unpublished
            2 (bases 1 to 2672)
            Fujii,Y., Takayama,K., Tsuritani,K., Yajima,Y., Amemiya,T.,
            Uka,Y., Naito,K. and Kawaguchi,A.
            Direct Submission
            Submitted (12-MAY-1999) Yasuyuki Fujii, Taisho Pharmaceutical Co.,
            Ltd., Molecular Biology Laboratory, Yoshino-cho, 1-403, Ohmiya,
            Saitama 3308530, Japan (E-mail: s17561@ccm.taisho.co.jp,
            Tel:+81-48-663-1111, Fax:+81-48-652-7254)
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            IYTKALGQANESHSNGSILPIISWRGSDMTFCVARNPVSRNFSPLIARLCEGA
            ADDPDSNVILICLIVPLLSFLVGLFLMPFKRQERYIEKKRVDICRETPNICP
            HSGENTREYDITPHNRTILKEDPANTVSTVEIPKMNPHSLITWDPTRPLFAVENV
            I"

FEATURES
source
1..2672

CDS
ORIGIN
Query Match      70.6%; Score 1910; DB 9; Length 2672;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2010; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      147 GCGGTAGCTTCCCTCTGAGAGTCCAAAGTGAAGCAAGTTGACTCTATGTTGACCTTC 206
Db      121 GCGGTAGCTTCCCTCTGAGAGTCCAAAGTGAAGCAAGTTGACTCTATGTTGACCTTC 180
Qy      207 AACACAAACCCCTTTTTCACATACAGCCAGAAAGGGGGGCACTATCATAGTACCCAAAT 266
Db      181 AACACAAACCCCTTTTTCACATACAGCCAGAAAGGGGGGCACTATCATAGTACCCAAAT 240
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QY 1347 ATGCAAGGTACACATTTATATGACGCTGTTGTTAATGATGCTCCAGGTCACTGT 1406
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Db 1321 ATGCAAGGTACACATATTAATGACGCTGTTGTTAATTAATGATGCTCCAGTCACTGT 1380
QY 1407 CTGAGTTTCATTTCCATCCAGGGCTGGATGTCAGATTAATACCAAGGCTTGCTACC 1466
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Db 1441 AGGAGGGCAAGAGACCAAAACAGACAGACAGAGTCCAGAGAGAGATGACCTGACAA 1500
QY 1527 AATGATGATTAATTAATGCTCTATTAATATATGTCCTCAGCATCTGCTGACCTTACCT 1586
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Db 1861 CCAATTAAGAGACCGAGTCTGAAGTCAATTTAATTAAGTGTAGAGACTTGAAGTCA 1920
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Db 1921 GGCAGTGAAGTGTGAGGAG 1980
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Db 1981 AATTCATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2012

RESULT 3
BD249810 2774 bp DNA linear PAT 17-JUL-2003
LOCUS 33 human secreted proteins.
DEFINITION BD249810
ACCESSION BD249810.1 GI:33059580
VERSION JP 2002540763-A/12.
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2774)
Moore,P.A., Shi,Y., Lafleur,D.W., Olsen,H.S., Florence,K.A. and Komatsoulis,G.
33 human secreted proteins
Patent: JP 2002540763-A 12 03-DEC-2002;
TITLE HUMAN GENOME SCIENCES INC
JOURNAL
COMMENT
OS Homo sapiens (human)
PN JP 2002540763-A/12
PD 03-DEC-2002
PF 08-FEB-2000 JP 2000598519
PR 10-FEB-1999 US 60/119468
PI CRAIG A ROSEN, STEVEN M RUBEN, REINHARD EBNER, PAUL E YOUNG, JIAN
NI,
PI DANIEL R SOPPET, PAUL A MOORE, YANGU SHI, DAVID W LAFLEUR, HENRIK

PI S OLSEN
 PI KIMBERLY A FLORENCE GEORGE KOMATSULIS
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 QY 61 GCCTCACCCTCATCTATATCTCTTGGAGCTCAGAGGCTGAGAGCTTGGAGCCCTGA 120
 DB 73 GCCTCACCCTCATCTATATCTCTTGGAGCTCAGAGGCTGAGAGCTTGGAGCCCTGA 132
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 DB 1573 GCCCAGCAGATGCTGAGCTTCACTTAATTTGTCAGAGCTGCTGCTGCTCATTAAT 1632

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Db 1993 GTACTGTAAACCTTTAAAGATGTTAATTCATTCAATAGATATTTATTAGAACC 2048
| | | | |

RESULT 4
HSM805512 2445 bp mRNA linear PRI 12-JUL-2002
LOCUS HSM805512
DEFINITION Homo sapiens mRNA; cDNA DKFp667F126 (from clone DKFZp667F126).
ACCESSION AL834424
VERSION AL834424.1 GI:21740141
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2445)
Bloeker,H., Boecher,M., Brandt,P., Mewes,H.W., Well,B. and Wiemann,S.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp667F126) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.

FEATURES

source

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35..721
/note="similarity to 19A24 (Homo sapiens)"
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ORIGIN

Query Match 58.1%; Score 1571; DB 9; Length 2445;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 417 GAGCACTGTCAAGCCTTAAGTCACTGAGGCTGACAGGCATTAAGATGGACCTGT 476
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QY 477 GTACCAATCTGACATGCTGACATGGAACATGAGGAAGATGATTTATACCTGAAG 536
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QY 537 GCCCTGGGGCAAGCAGCCCAATGATCCCAATATGGGTCATCTCTCCCATCTCTGGAGA 596
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Qy 1317 GTGCTTGAAGATTTCCATATGAATGAATGAAGTGCACATATTAATGACAGCT 1376

Db 989 GTGCTTGAAGATTTCCATATGAATGAATGAAGTGCACATATTAATGACAGCT 1048

Qy 1377 GTTGTATTAATGATGCTGCTCAGATGCTGAGATTTCAATTCATCCAGGCTTGA 1436

Db 1049 GTTGTATTAATGATGCTGCTCAGATGCTGAGATTTCAATTCATCCAGGCTTGA 1108

Qy 1437 TGTGAGATTAATCAAGAGTCTTGTCTACAGAGGCGCAGAGACCAAAACAGACAG 1496

Db 1109 TGTGAGATTAATCAAGAGTCTTGTCTACAGAGGCGCAGAGACCAAAACAGACAG 1168

Qy 1497 AAGTCCAGAGACAGATGACCTGACAAATGATTAATGCTTAACT 1556

Db 1169 AAGTCCAGAGACAGATGACCTGACAAATGATTAATGCTTAACT 1228

Qy 1557 ATGTGCCAGACATATGCTGCTTAACTTAACTTAACTTAACTTAACT 1616

Db 1229 ATGTGCCAGACATATGCTGCTTAACTTAACTTAACTTAACTTAACT 1288

Qy 1617 AATGCTCTCAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 1676

Db 1289 AATGCTCTCAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 1348

Qy 1677 TTCCAGAGGCGCAGATGCTGCTTAACTTAACTTAACTTAACTTAACT 1736

Db 1349 TTCCAGAGGCGCAGATGCTGCTTAACTTAACTTAACTTAACTTAACT 1408

Qy 1737 AATCAGGCTGATGCTGCTTAACTTAACTTAACTTAACTTAACTTAACT 1796

Db 1409 AATCAGGCTGATGCTGCTTAACTTAACTTAACTTAACTTAACTTAACT 1468

Qy 1797 CCCAAGACAGAGCTGCTGCTTAACTTAACTTAACTTAACTTAACTTAACT 1856

Db 1469 CCCAAGACAGAGCTGCTGCTTAACTTAACTTAACTTAACTTAACTTAACT 1528

Qy 1857 CTAGCTTAAAGCTGCTGCTTAACTTAACTTAACTTAACTTAACTTAACT 1916

Db 1529 CTAGCTTAAAGCTGCTGCTTAACTTAACTTAACTTAACTTAACTTAACT 1588

Qy 1917 TGTAAATCTAGTAGAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1976

Db 1589 TGTAAATCTAGTAGAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1648

Qy 1977 GTGGGTAATCTGTAACCTTTAAGATGCTTAACTTAACTTAACTTAACTTAACT 2036

Db 1649 GTGGGTAATCTGTAACCTTTAAGATGCTTAACTTAACTTAACTTAACTTAACT 1708

Qy 2037 TA 2038

Db 1709 TA 1710

RESULT 5
LOCUS AF390894 1352 bp mRNA linear PRI 02-NOV-2001
DEFINITION Homo sapiens CD2-like receptor activating cytotoxic cells mRNA,
complete cds.
ACCESSION AF390894
VERSION AF390894.1 GI:16589010
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1352)
Bouchon,A., Cella,M., Grierson,H.L., Cohen,J.I. and Colonna,M.

TITLE Cutting Edge: Activation of NK Cell-Mediated Cytotoxicity by a
SNP-Independent Receptor of the CD2 Family
JOURNAL J. Immunol. 167 (2001) In press
REFERENCE 2 (bases 1 to 1352)
AUTHORS Colonna,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2001) Basel Institute for Immunology, 487
Grenzacherstrasse, Basel CH-4005, Switzerland
FEATURES
Source
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ORIGIN

Query Match 46.7%; Score 1264; DB 9; Length 1352;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 22 GCTGACTTCAGAGAGCAATATGCTGCTTCCCAACATGCTCACCCTCATATATCC 81

Db 1 GCTGACTTCAGAGAGCAATATGCTGCTTCCCAACATGCTCACCCTCATATATCC 60

Qy 82 TTGGGAGCTCACAGGCTGACAGCTCTGGAACCGTGAAGAAGCTGGTCCGTTG 141

Db 61 TTGGGAGCTCACAGGCTGACAGCTCTGGAACCGTGAAGAAGCTGGTCCGTTG 120

Qy 142 GTGGGCGCTGACTTTTCCCTGAAGTCCAAAGTAAGCAAGTGAATGCTATGTCGA 201

Db 121 GTGGGCGCTGACTTTTCCCTGAAGTCCAAAGTAAGCAAGTGAATGCTATGTCGA 180

Qy 202 CCTTCAACACACCCCTCTTGTACCATACAGCCAGAGAGGCGCATATCATATGTCGCC 261

Db 181 CCTTCAACACACCCCTCTTGTACCATACAGCCAGAGAGGCGCATATCATATGTCGCC 240

Qy 262 AAATGCTAATAGAGAGAGTGAAGTCTCCAGATGAGGCTATCTCCCTGAAGCTCAGCA 321

Db 241 AAATGCTAATAGAGAGAGTGAAGTCTCCAGATGAGGCTATCTCCCTGAAGCTCAGCA 300

Qy 322 AACTGAAGAAGATGACTCAGGATCTATATGTGGGATATACAGTCTATCTCAGC 381

Db 301 AACTGAAGAAGATGACTCAGGATCTATATGTGGGATATACAGTCTATCTCAGC 360

Qy 382 AGCCCTCACCGAGAGTATGCTGCTGATGCTTACAGAGCACTGTCAAAAGCTTAAAGTCA 441

Db 361 AGCCCTCACCGAGAGTATGCTGCTGATGCTTACAGAGCACTGTCAAAAGCTTAAAGTCA 420

Qy 442 CCATGGGTGTCAGAGCAATGAATGAGCACTGTGTGAACCAATGCAATGCTGATGG 501

Db 421 CCATGGGTGTCAGAGCAATGAATGAGCACTGTGTGAACCAATGCAATGCTGATGG 480

Qy 502 AACATGGGGAAGAGATGATTTATTAATCTGGAAGGCGCTGGGGCAGAGCCCAATGAGT 561

Db 481 AACATGGGGAAGAGATGATTTATTAATCTGGAAGGCGCTGGGGCAGAGCCCAATGAGT 540

Qy 562 CCATATATGGGTCAATCTCTCCATCTCTGAGATGGGAGAAAGTATATGACTTCA 621

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Db 541 CCCATATGGGTCATCTCCATCCCTCCGAGATGGGAGAAAGATATACCTTCA 600
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Qy 682 TCTGTGAAGGTGCTGTGATGAGACCAGATTCTCTCATGTGCTCTGTGTCTCTGTGG 741
Db 661 TCTGTGAAGGTGCTGTGATGAGACCAGATTCTCTCATGTGCTCTGTGTCTCTGTGG 720
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Db 721 TGGCCCTCTCTGCTCACTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGA 780
Qy 802 GACAGAAGAGTACATTTGAAGAGAAGAGAGTGGACATTTGTGGGAAACTCTTAACA 861
Db 781 GACAGAAGAGTACATTTGAAGAGAAGAGAGTGGACATTTGTGGGAAACTCTTAACA 840
Qy 862 TATGCCCCCATCTTGTGAGAGACACAGATGACACAATCCCTCACACTAATAGAACAA 921
Db 841 TATGCCCCCATCTTGTGAGAGACACAGATGACACAATCCCTCACACTAATAGAACAA 900
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Db 901 TCTTAAAGGAAGTCCAGCAATACGCTTATCTCTCACTGTGAAATTCGGAAGAGATG 960
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Qy 1162 ACGTGACTTTTCCAGATAAATTATCTGTAGTCTTCTTGAATTTAAGATTGGTA 1221
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Qy 1282 AATGGGATTGTGAATGTCAAGCAACCATTAATAAAGTGTGTTAGAATTTCTTAT 1336
Db 1261 AATGGGATTGTGAATGTCAAGCAACCATTAATAAAGTGTGTTAGAATTTCTTAT 1315

RESULT 6
AR252549 1076 bp DNA linear PAT 20-DEC-2002
LOCUS AR252549 Sequence 252 from patent US 6478825.
DEFINITION AR252549
ACCESSION AR252549
VERSION AR252549.1 GI:27300457
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1076)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the
JOURNAL treatment of bone defects
FEATURES Patent: US 6478825-A 252 12-NOV-2002;
Location/Qualifiers
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ORIGIN

Query Match 39.8%; Score 1076; DB 6; Length 1076;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 GTGGCTTCAATTCAGTGGCTGACTTCCAGAGAGCAATATGGTGGTTCCTCCCAATGCTT 64
Db 1 GTGGCTTCAATTCAGTGGCTGACTTCCAGAGAGCAATATGGTGGTTCCTCCCAATGCTT 60
Qy 65 CACCTCATCTATATCTTTGGCAGCTCAAGAGTCAAGAGCTCTGAGCCCGTAAAGA 124
Db 61 CACCTCATCTATATCTTTGGCAGCTCAAGAGTCAAGAGCTCTGAGCCCGTAAAGA 120
Qy 125 GCTGTGGGTTCCGTTGGTGGGCGGTGAATTTCCCTGAAATCAAGTAAAGCAACT 184
Db 121 GCTGTGGGTTCCGTTGGTGGGCGGTGAATTTCCCTGAAATCAAGTAAAGCAACT 180
Qy 185 TGAATCTATATTTCTGGAACCTTCAACAAACCCCTTTGTACCATATACGCCGAAGGGG 244
Db 181 TGAATCTATATTTCTGGAACCTTCAACAAACCCCTTTGTACCATATACGCCGAAGGGG 240
Qy 245 CACTATCATATGAGCCCAAAATCGTAATAGGAGAGATGAGACTTCCAGATGAGGCTA 304
Db 241 CACTATCATATGAGCCCAAAATCGTAATAGGAGAGATGAGACTTCCAGATGAGGCTA 300
Qy 305 CTCCCTGAAGCTCAGCAAACTGGAAGAATGACTCAAGGATCTATATGTGGGATATA 364
Db 301 CTCCCTGAAGCTCAGCAAACTGGAAGAATGACTCAAGGATCTATATGTGGGATATA 360
Qy 365 CAGCTCATATCTCCAGAGCCCTCCACCCAGAGATACGTGCTGCAATGTTTACAGACACT 424
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Db 841 TCGGGAACCTCTTAATATATGCCCCCATCTTGTGAGAGAACACAGATACACATATCC 900
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Qy 1025 ATTGCTATATGAAATGTTATCTAGACAGAGCTGCACTCCCTAAGTCTTGCTCA 1080

Db 1021 ATTGGCTATGAGATGTTATCTAGACAGAGTGACCTCCCTTAAGTCTGCTCA 1076
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RESULT 7
AX092314 1076 bp DNA linear PAT 21-MAR-2001
LOCUS Sequence 45 from Patent WO0116318.
DEFINITION AX092314
ACCESSION AX092314
VERSION AX092314.1 GI:13444471
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Batton,D.L., Pilvaroff,B., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 45 08-MAR-2001;
Genentech, Inc. (US)
LOCATION/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 39.8%; Score 1076; DB 6; Length 1076;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GTGGCTTCATTTCAGTGGCTGACTTCCAGAGACAATATGGCTGTTCCCAACATGCT 64
DB 1 GTGGCTTCATTTCAGTGGCTGACTTCCAGAGACAATATGGCTGTTCCCAACATGCT 60
QY 65 CACCTTCATCTATATCTTTGGAGCTCAGAGGCTCAGCAGCTCTTGACCCCGTGAAGA 124
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DB 121 GCTGTGCGTTCCGTTGGTGGGCGCGTGAATTTCCCTGAAAGTCAAGTGAAGCAAGT 180
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DB 421 GTCAAAGCTTAAATCAACATGGGTCTGCAAGACAAATGAATGGACCTGTGTGACCA 480
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DB 541 GCAAGCAGCCATAGTCCCAATATGGGTCCATCTCCCAATCTCTGGAAGTGGGAGA 600

QY 605 AAGNATATGACCTTCATCTGGGTTGCAGGAACCCGTGAGAGAACTTCAAGCCC 664
DB 601 AAGNATATGACCTTCATCTGGGTTGCAGGAACCCGTGAGAGAACTTCAAGCCC 660
QY 665 CATCTTTGCCAGAGAGCTCTGTAGAGGTGCTGTATGACCCAGATTCCTCAATGCTCT 724
DB 661 CATCTTTGCCAGAGAGCTCTGTAGAGGTGCTGTATGACCCAGATTCCTCAATGCTCT 720
QY 725 CTTGTGCTCTCTGTTGGTCCCTCTCTGCTCACTCTCTTTGTAAGTGGGCTATTTCTTGG 784
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DB 781 GTTTTGAAGAGAGAGACAAGATGATGATGAAAGAAAGAGAGTGAATTTG 840
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DB 841 TCGGGAACCTCTTACATATGCCCCCATCTTGAGAGAACACAGAGTACACAAATCCC 900
QY 905 TCACTATATGAAACAATCTTAAGAGATCCAGCAATACGTTTACTCTCACTGTGA 964
DB 901 TCACTATATGAAACAATCTTAAGAGATCCAGCAAAATACGTTTACTCTCACTGTGA 960
QY 965 AATACGGAAGAAAGATGAAATCCCACTCACTGCTCAGATGCCAGACACCAAGGCT 1024
DB 961 AATACGGAAGAAAGATGAAATCCCACTCACTGCTCAGATGCCAGACACCAAGGCT 1020
QY 1025 ATTGGCTATGAGATGTTATCTAGACAGAGTGCACTCCCTTAAGTCTGCTCA 1080
DB 1021 ATTGGCTATGAGATGTTATCTAGACAGAGTGCACTCCCTTAAGTCTGCTCA 1076
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RESULT 8
AX376124 1076 bp DNA linear PAT 01-MAR-2002
LOCUS Sequence 191 from Patent WO0168848.
DEFINITION AX376124
ACCESSION AX376124
VERSION AX376124.1 GI:19170454
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
Zhang,Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 191 20-SEP-2001;
Genentech, Inc. (US)
LOCATION/Qualifiers
FEATURES
source 1..1076
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GTGGCTTCATTTCAGTGGCTGACTTCCAGAGACAATATGGCTGTTCCCAACATGCT 64
DB 1 GTGGCTTCATTTCAGTGGCTGACTTCCAGAGACAATATGGCTGTTCCCAACATGCT 60
QY 65 CACCTTCATCTATATCTTTGGAGCTCAGAGGCTCAGCAGCTCTTGACCCCGTGAAGA 124
DB 61 CACCTTCATCTATATCTTTGGAGCTCAGAGGCTCAGCAGCTCTTGACCCCGTGAAGA 120
QY 125 GCTGTGCGTTCCGTTGGTGGGCGCGTGAATTTCCCTGAAAGTCAAGTGAAGCAAGT 184

Db 121 GCTGTCGCTTCCGTTGGTGGGCGCGTACCTTCCCTCAAGTCCAAATGAAGCAAGT 180
Qy 185 TGAAGTATGTTGTCGACCTTCAACACACCCCTTTGTGACCAATACAGCCAGCAAGGGG 244
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Qy 245 CAGTATCATAGTGAAGCCAAATGTAATAGAGAGAGTACCTTCCAGATGAGGCTA 304
Db 241 CAGTATCATAGTGAAGCCAAATGTAATAGAGAGAGTACCTTCCAGATGAGGCTA 300
Qy 305 CTCCCTGAAGCTCAGCAAACTGAAGAAATGACTCAGGAGTCTACTATGTGGGATATA 364
Db 301 CTCCCTGAAGCTCAGCAAACTGAAGAAATGACTCAGGAGTCTACTATGTGGGATATA 360
Qy 365 CAGCTCATCATCAGAGGCGCTCCACCCAGAGAGTACGTCGATGCTTCAAGAGCACT 424
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Qy 425 GTCAAAAGCTTAAAGTCAACATGGGTCTGACAGCAATAGCAATGCACTGTGTACCA 484
Db 421 GTCAAAAGCTTAAAGTCAACATGGGTCTGACAGCAATAGCAATGCACTGTGTACCA 480
Qy 485 TCTGACATGCTGCATGGAACATGGGGAAGAGATGTGATTTATACCTGGAAGGCTGTGG 544
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LOCUS AX403365
DEFINITION Sequence 252 from Patent WO0073454.
ACCESSION AX403365
VERSION AX403365.1 GI:21436903
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Eaton, D.,
Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,
Grimaldi, C.J., Gurney, A.L., Kijavits, I., Napier, M.A., Pan, J.,
Paoletti, N.F., Roy, M., Stewart, T.A., Tunes, D., Watanabe, C.K.,
Williams, P., Wood, W.I. and Zhang, Z.
TITLE
Secreted and transmembrane polypeptides and nucleic acid encoding
the same
JOURNAL
Patent: WO 0073454-A 252 07-DEC-2000;
Genentech Inc. (US)
FEATURES
source
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 GTGGCTTCAATTCAGTGGCTGACCTTCAGAGAGCAATATGCTGTTCCCAACATGCTT 64
Db 1 GTGGCTTCAATTCAGTGGCTGACCTTCAGAGAGCAATATGCTGTTCCCAACATGCTT 60
Qy 65 CACCCATCATATATCTTCTTGGCAGCTCAGAGGTCAGAGGCTGAGCCCTGAGAAAGA 124
Db 61 CACCCATCATATATCTTCTTGGCAGCTCAGAGGTCAGAGGCTGAGCCCTGAGAAAGA 120
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Db 181 TGAAGTATGTTGTCGACCTTCAACACACCCCTTTGTGACCAATACAGCCAGAAAGGGG 240
Qy 245 CAGTATCATAGTGAAGCCAAATGTAATAGAGAGAGTACCTTCCAGATGAGGCTA 304
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RESULT 11
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LOCUS Homo sapiens mRNA, cDNA DKFZp667N1110 (from clone DKFZp667N1110).
DEFINITION AL713801
ACCESSION AL713801.1 GI:19584564
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 3532)
AUTHORS Duesterhoeft, A., Lauber, J., Mewes, H.W., Weil, B. and Wiemann, S.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-2002) MIPS, Am Klopferespitz 18a, D-82152 Martinsried, GERMANY

COMMENT
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de; sequenced by Olagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp667N1110) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further information about the clone and the sequencing project is available at <http://mips.gsf.de/proj/cdna/>.

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3511
polya_site

ORIGIN
Query Match 39.7%; Score 1073; DB 9; Length 3532;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1035 GAGAAATGTTATCTAGACAGAGTGCACTGCCCTTAAGTCTTGCTCAAAAAACAATT 1094
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QY 1095 CTCGGCCCAAGAAAACAATCAGAAAGATTCACTGATTTGACTAGAAACATCAAGAGA 1154
DB 1924 CTCGGCCCAAGAAAACAATCAGAAAGATTCACTGATTTGACTAGAAACATCAAGAGA 1983

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QY 1215 GTTCGTAATTCATCCACTGCTGAGAAAATCTCTCAAAACCCAGAGGTTTAATCACTTCA 1274
DB 2044 GTTCATTAATTCATCCACTGCTGAGAAAATCTCTCAAAACCCAGAGGTTTAATCACTTCA 2103

QY 1275 TCCCAAAAATGGGATTTGAAATGTCAGCAAAACCATTAATAAAAGTCTTGAAGATTTCT 1334
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QY 1395 CCAGGTGAGTGTCTGAGATTTTCATTCCATCCAGAGGCTTGAATGTCAGATTATACCAAG 1454
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QY 1455 AGTCTTGCTACCAAGAGGGCAAGAACCAAAACAGACAGCAAGTCCAGCAAGACACA 1514
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QY 1515 TGCACCTGACAAAATGATGATTAATTGGCTCTATAAATGATGTCACAGCACTATGC 1574
DB 2344 TGCACCTGACAAAATGATGATTAATTGGCTCTATAAATGATGTCACAGCACTATGC 2403

QY 1575 TGAGCTTACACTAATTTGTCAGACGCTGCTGCTCATGAAATTTGCTTCAATGAA 1634
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QY 1875 CCAGAACCCATCCCAATTAAGAGACCGAGTCCGAAGTCAATTTGAATCTAGTAGGA 1934
DB 2704 CCAGAACCCATCCCAATTAAGAGACCGAGTCCGAAGTCAATTTGAATCTAGTAGGA 2763

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DB 2764 GACTTGAGTCAAGCAGTGAAGCTGTGTGGGCAACGGGGGCGATGGGTACTTTAACT 2823

QY 1995 TTAAGATGTTAATTTCAATTCATATGATATTTATTAAAGCTTA 2038
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RESULT 12
AR252550 1053 bp DNA linear PAT 20-DEC-2002
LOCUS AR252550
DEFINITION Sequence 254 from patent US 6478825.
ACCESSION AR252550
VERSION AR252550.1 GI:27300458
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1053)
AUTHORS Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.
TITLE Implant, method of making same and use of the implant for the treatment of bone defects
JOURNAL Patent: US 6478825-A 254 12-NOV-2002;

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Source Location/Qualifiers
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Query Match 38.6%; Score 1044; DB 6; Length 1053;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1044; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 CTGGTTCCTCCCAACATGCTCTCACTCTATCTATCTCTTGGCAGCTCAGAGGCTCAG 105
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QY 706 CAGATTCCTCATGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
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QY 1006 TGGCAGACACACCAAGGCTATTTGGCTATGAGATGTTATCTAGACAGAGTGCACCTCCC 1065
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RESULT 13
AX403367 1053 bp DNA linear PAT 14-JUN-2002
LOCUS AX403367
DEFINITION Sequence 254 from Patent WO0073454.
ACCESSION AX403367
VERSION AX403367.1 GI:21436904
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Eaton, D.,
Ferrara, N., Gerber, H., Gerltzen, M., Goddard, A., Godowski, P.,
Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J.,
Pao, N.F., Roy, M., Stewart, T.A., Tumes, D., Watanabe, C.K.,
Williams, P., Wood, W.I. and Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0073454-A 254 07-DEC-2000;
Genentech Inc. (US)

JOURNAL

FEATURES
Source Location/Qualifiers
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ORIGIN

Query Match 38.6%; Score 1044; DB 6; Length 1053;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1044; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 CTGGTTCCTCCCAACATGCTCTCACTCTATCTATCTCTTGGCAGCTCAGAGGCTCAG 105
DB 1 CTGGTTCCTCCCAACATGCTCTCACTCTATCTATCTCTTGGCAGCTCAGAGGCTCAG 60
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| | | | |
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| | | | |
DB 1021 CTAAGTCTCTGCTCAAAAAA 1044
| | | | |

RESULT 14
BD249841 2780 bp DNA linear PAT 17-JUL-2003
LOCUS 33 human secreted proteins.
DEFINITION BD249841
ACCESSION BD249841.1 GI:33059611
VERSION JP 2002540763-A/43.
KEYWORDS JP 2002540763-A/43.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2780)
AUTHORS Rosen,C.A., Ruben,S.M., Ebner,R., Young,P.E., M.J., Soppet,D.R.,
Moore,P.A., Shi,Y., Lafleur,D.W., Olsen,H.S., Florence,K.A. and
Komatsoulis,G.
TITLE 33 human secreted proteins
JOURNAL Patent: JP 2002540763-A 43 03-DEC-2002;
HUMAN GENOME SCIENCES INC
COMMENT OS Homo sapiens (human)
PN JP 2002540763-A/43
PD 03-DEC-2002
PR 08-FEB-2000 JP 2000598519
PI 10-FEB-1999 US 60/119468
PI CRAIG A ROSEN, STEVEN W RUBEN, REINHARD EBNER, PAUL E YOUNG, JIAN
NI,
PI DANIEL R SOPPET, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR, HENRIK
PI S OLSEN,
PI KIMBERLY A FLORENCE, GEORGE KOMATSOUKIS
PC C12N15/09, A61K31/7115, A61K38/00, A61K48/00, A61P1/00, A61P1/04,
A61P1/16,

PC A61P3/12, A61P5/10, A61P7/00, A61P7/04, A61P7/06, A61P9/00, A61P9/10, PC
A61P11/06,
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PC C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10 PC
, C12P21/02, C12Q1/02,
PC C12Q1/68, C01G01N33/15, G01N33/50, G01N33/53, G01N33/53, G01N33/566,
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PC A61K37/02, C12N5/00
CC 33 human secreted proteins
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Qy 1610 CTTTCATGAAATGGCTCTCAAAATGATGAACTACTTTTCATGAGCACTTGTGACAGGCTG 1669

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Qy 2030 AAGAACCTAC 2039

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RESULT 15

AF291815

LOCUS AF291815 1083 bp mRNA linear PRI 13-NOV-2001

DEFINITION Homo sapiens NK cell receptor (CS1) mRNA, complete cds.

ACCESSION AF291815.1 GI:13021809

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 1083)

REFERENCE

AUTHORS

TITLE

Molecular cloning of CS1, a novel human natural killer cell

receptor belonging to the CD2 subset of the immunoglobulin

superfamily

Immunogenetics 52 (3-4), 302-307 (2001)

JOURNAL

MEDLINE

PUBMED

1120635

2 (bases 1 to 1083)

REFERENCE

AUTHORS

TITLE

Boles,K.S. and Mathew,P.A. Sr.

Direct Submision

Submitted (01-AUG-2000) Molecular Biology and Immunology, UNT

Health Science Center, 3500 Camp Bowie Blvd, Fort Worth, TX 76107,

USA

FEATURES

source

Location/Qualifiers

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ADDPDSNVLLCLLIVPLSLFVLGLPLMFLRREOEYIEEKQVDICRETPNICP

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ORIGIN

Query Match

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 91 TCACAGGCTCAGAGCCTCTGACCCGTGAAGAGCTGGTCCGTTGGTGGGCGC 150

Db 61 TCACAGGCTCAGAGCCTCTGACCCGTGAAGAGCTGGTCCGTTGGTGGGCGC 120

Qy 151 TGACTTTCCCTGAAATCCAAAGTAAAGCAATGACTTATGTCGAGACCTTCACA 210

Db 121 TGACTTTCCCTGAAATCCAAAGTAAAGCAATGACTTATGTCGAGACCTTCACA 180

Qy 211 CAACCCCTTTGTACCATTAACAGCCAGAGGCGCACTATCATATGAGACCAAAATGTA 270

Db 181 CAACCCCTTTGTACCATTAACAGCCAGAGGCGCACTATCATATGAGACCAAAATGTA 240

Qy 271 ATAGGAGAGATGAGATCTCCAGATGAGGCTAATCCCTGAAGCTCAGAACTGAGA 330

Db 241 ATAGGAGAGATGAGATCTCCAGATGAGGCTAATCCCTGAAGCTCAGAACTGAGA 300

Qy 331 AGAATGACTCAGGATCTAATATGAGGAGATATACAGCTCATCTCCACAGCCCTCA 390

Db 301 AGAATGACTCAGGATCTAATATGAGGAGATATACAGCTCATCTCCACAGCCCTCA 360

Qy 391 CCCAGAGATGAGTGTGATGCTGATGCTGATGATGATGATGATGATGATGATGATG 450

Db 361 CCCAGAGATGAGTGTGATGCTGATGCTGATGATGATGATGATGATGATGATGATG 420

Qy 451 TGCAGAGCAATAGATGAGTGTGATGCTGATGATGATGATGATGATGATGATGATG 510

Db 421 TGCAGAGCAATAGATGAGTGTGATGCTGATGATGATGATGATGATGATGATGATG 480

Qy 511 AAGAGATGATTTATTAATCTGGAAGGCTCTGGGAGAGCAATGAGTCCCATATG 570

Db 481 AAGAGATGATTTATTAATCTGGAAGGCTCTGGGAGAGCAATGAGTCCCATATG 540

Qy 571 GGTCACTCTCCCATCTCTCTGAGATGGGAGAGAGATGATGATGATGATGATGATG 630

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Db 781 AGTACATTTGAAG 840

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RESULT 16
AC068728
LOCUS
DEFINITION
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5 unordered pieces.
AC068728 AC068728.7 GI:13174202
VERSION
KEYWORDS
SOURCE HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
ORGANISM Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 166345)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Federspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Lam,B., Marathe,R., Miranda,M., Morehouse,A.J., Nguyen,M.,
Oefner,P., Palm,C.J., Ramirez,D., Southwick,A.M., Wilhelmly,J.,
Yu,S. and Davis,R.W.
Unpublished
2 (bases 1 to 166345)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Federspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J.,
Ramirez,D., Wilhelmly,J., Yu,S. and Davis,R.W.
Direct Submission
Submitted (08-MAY-2000) DNA Sequencing and Technology Center
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
On Mar 1, 2001 this sequence version replaced gi:11878529.
----- Genome Center
Center: Stanford DNA Sequencing and Technology Development
Center
Center code: SDSTDC
Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
----- Project Information
Center clone name: RP11-BD14
----- Summary Statistics
Sequencing Vector: M13mp18; X02513
Chemistry: Dye-Primer; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 160988 bases at least Q40
Consensus quality: 161717 bases at least Q30
Consensus quality: 161956 bases at least Q20
Insert size: 164605; agarose-fp
Insert size: 165945; sum-of-contigs
Quality coverage: 9.0x in Q20 bases; agarose-fp
Quality coverage: 8.9x in Q20 bases; sum-of-contigs.
NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1866: contig of 1866 bp in length
* 1867 1966: gap of unknown length
* 1967 3797: contig of 1831 bp in length
* 3798 3898: gap of unknown length
* 3898 23083: contig of 19186 bp in length
* 23084 23183: gap of unknown length
* 23184 62924: contig of 39741 bp in length
* 62925 63025: gap of unknown length
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RESULT 17
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LOCUS BD249842 1412 bp DNA linear PAT 17-JUL-2003
DEFINITION 33 human secreted proteins.
ACCESSION BD249842
VERSION BD249842.1 GI:33059612
KEYWORDS JP 2002540763-A/44.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1412)
Rosen,C.A., Ruben,S.M., Ebnert,R., Young,P.E., Ni,J., Soppet,D.R.,
Moore,P.A., Shi,Y., Lafleur,D.W., Olsen,H.S., Florence,K.A. and
Komatsoulis,G.
33 human secreted proteins
Patent: JP 2002540763-A 44 03-DEC-2002;
HUMAN GENOME SCIENCES INC
OS Homo sapiens (human)
PN JP 2002540763-A/44
PD 03-DEC-2002
PR 08-FEB-2000 JP 2000598519
PR 08-FEB-1999 US 60/119468
PI CRAIG A ROSEN,STEVEN M RUBEN,REINHARD EBNER,PAUL E YOUNG,JIAN
NI,
PI DANIEL R SOPPET,PAUL A MOORE,YANGU SHI,DAVID W LAFLEUR,HENRIK

TITLE
JOURNAL
COMMENT

PC A61P25/18, A61P25/24, A61P25/28, A61P27/02, A61P31/04, A61P31/18,
PC A61P35/00
PC A61P35/02, A61P37/00, A61P37/02, A61P37/06, A61P37/08, A61P43/00,
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, C12P21/02, C12Q1/02,
PC C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/53, G01N33/56,
PC C12N15/00
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Best Local Similarity 99.6%; Pred. No. 0;
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QY 1636 GAACTACTTTCATGAGCAGTGTGAGCAGGCTGACCAAGATTCAGAGGAGGAGATGCT 1695
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DEFINITION 87 human secreted proteins.
ACCESSION BD082372
VERSION BD082372.1 GI:22627982
KEYWORDS JP 2001522239-A/14.
SOURCE Mastadenovirus
ORGANISM Mastadenovirus
Virus; dsDNA viruses, no RNA stage; Adenoviridae.
1 (bases 1 to 1412)
AUTHORS Young, P., Greene, J.M., Ferrite, A.M., Ruben, S.M., Rosen, C.A.,
Duan, R.D., Hu, J.S., Florence, K.A., Olsen, H.S., Ebner, R.,
Breuer, L.A., Moore, P.A., Shi, Y., Lafleur, D.W. and Ni, U.
87 human secreted proteins
Patent: JP 2001522239-A 14 13-NOV-2001;
HUMAN GENOME SCIENCES INC SECRETARY OF THE DEPARTMENT OF HEALTH
HUMAN SERVICES
PN JP 2001522239-A/14
COMMENT
PD 13-NOV-2001
PR 19-MAR-1998 JP 1998542119
PR 21-MAR-1997 US 60/041281, 21-MAR-1997 US 60/041276 PR
30-MAY-1997 US 60/042344, 21-MAR-1997 US 60/041277 PR
30-MAY-1997 US 60/048355, 30-MAY-1997 US 60/048096 PR
30-MAY-1997 US 60/048351, 30-MAY-1997 US 60/048154 PR
30-MAY-1997 US 60/048160, 30-MAY-1997 US 60/048069 PR
30-MAY-1997 US 60/048131, 30-MAY-1997 US 60/048186 PR

30-MAY-1997 US 60/048095, 30-MAY-1997 US 60/048187 PR
30-MAY-1997 US 60/048099, 30-MAY-1997 US 60/050937 PR
30-MAY-1997 US 60/048352, 30-MAY-1997 US 60/048135 PR
30-MAY-1997 US 60/048188, 30-MAY-1997 US 60/048094 PR
30-MAY-1997 US 60/048350, 05-AUG-1997 US 60/054804 PR
19-AUG-1997 US 60/056370, 02-OCT-1997 US 60/060862 PI
YOUNG, JOHN M GREENE, ANN M FERRIE, STEVEN M RUBEN, CRAIG A PI
ROSEN, ROXANNE D DUAN, JING SHAN HU, KIMBERLY A FLORENCE, HENRIK S
OLSEN, PI
REINHARD EBNER, LAURIE A BREWER, PAUL A MOORE, YANGSU SHI, DAVID W
PI
LAFLUR,
PI
JIAN NI
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C07K14/00
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Strandedness: Double;
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Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
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 Db 1321 ACTTGGAGTACGAGGAGTGAAGCTGTGGGGGACCGGGGGGCA 1361
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 LOCUS HSA276429
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 ACCESSION AJ276429
 VERSION AJ276429.2 GI:12619176
 KEYWORDS 19A gene; early response gene.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Murphy, J.J. and Norton, J.D.
 TITLE Cell type specific early response gene expression during
 plasmacytoid differentiation of human B lymphocytic leukaemia cells
 JOURNAL Blochim. Biophys. Acta 1049, 262-271 (1990)
 REFERENCE
 AUTHORS Murphy, J.J., Hobby, P., Vilarino-Varela, J., Bishop, B.,
 Jordanidou, P., Sutton, B.J. and Norton, J.D.
 TITLE A novel immunoglobulin superfamily receptor (19A) related to CD2 is
 expressed on activated lymphocytes and promotes homotypic B-cell
 adhesion
 JOURNAL Biochem. J. 361 (Pt 3), 431-436 (2002)
 MEDLINE 21661458

PUBMED 11802771
 REFERENCE 3
 AUTHORS Murphy, J.J.
 TITLE Direct Submission
 JOURNAL Submitted (17-MAR-2000) Murphy J.J., Division of Life Sciences,
 King's College London, 150 Stamford Street, London, SE1 8WA, UNITED
 KINGDOM
 REMARK revised by [3]
 REFERENCE 4 (bases 1 to 1111)
 AUTHORS Murphy, J.J.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-2001) Murphy J.J., Division of Life Sciences,
 King's College London, Franklin-Wilkins Building, 150 Stamford
 Street, London, SE1 9NN, UNITED KINGDOM
 COMMENT On Jan 30, 2001 this sequence version replaced gi:7320862.
 FEATURES
 source
 1. .1111
 /organism="Homo sapiens"
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 /db_xref="TrEMBL:O9NY08"
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 Query Match 34.4%; Score 930; DB 9; Length 1111;
 Best Local Similarity 99.8%; Pred. No. 0;
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QY	991	ACTCATCTGCTACGATGCGAGACACACCAAGGCTAATTTGCTATGAGATGTTATCTAGA	1050
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LOCUS	BC027867
DEFINITION	Homo sapiens SLAM family member 7, mRNA (cDNA clone MGC:34188
ACCESSION	BC027867
VERSION	BM927867.1
KEYWORDS	GI:20380756
SOURCE	MGC.
ORGANISM	Homo sapiens (human)
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 2658)
AUTHORS	Klausner,R.D., Collins,F.S., Wagner,L., Shemen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schacter,C.F., Bhattacharya,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Ditchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stepleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Ueda,T.B., Toshiyuki,S., Canciari,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mollahy,S.U., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Huylk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodríguez,A.C., Gilmwood,J., Schmitt,J., Myers,R.M.,

TITLE Buterfield, Y.S., Krzywinski, M.I., Skalske, U., Smalish, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
JOURNAL Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 22388257
PMID 12477932
REFERENCE 2 (bases 1 to 2658)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
 Email: gcgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web Site: <http://www.nisc.nih.gov/>
 Contact: ayce_mgc@nhgri.nih.gov
 Akhter, N., Nye, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Khong, P., Laric, P., Legaspi, R., Maduro, O.L., Masello, C., Meekel, B., Mastrrian, S.D., McCloskey, J.C., McDowall, J., Pearson, R., Statutis, S., Thomas, P.J., Touchman, J.W., Young, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.lnl.gov>
 Series: IRAC plate 49 Row: e Column: 22
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19923571.
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 Db 1861 TTAAGATGTTTATTCATTCATTAAGATATTTATTAAGAACCTA 1904

RESULT 21
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 leukemia-associated)) protein pseudogene, the CD48 gene for CD48
 antigen (B-cell membrane protein), the gene for a novel LY9
 (lymphocyte antigen 9) like protein and the 5' end of the LY9 gene.
 Contains ESTs, STSs and GSSs, complete sequence.
 AL121985
 AL121985.13 GI:7161187
 HTG; CD48; LY9; SET; SLAM.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 195976)
 Bases, K.
 Direct Submission
 Submitted (04-APR-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 requests: clonerquest@sanger.ac.uk
 On Mar 6, 2000 this sequence version replaced gi:6983370.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence has been finished according to sequence map criteria
 as follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known
 annotated human repeat sequence elements (e.g. Alu). Where the
 sequence is ambiguous, there is an annotation using the 'unsure'
 feature key.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information
 on the WORMPEP database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
 Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr1
 RP11-404F10 is from the library RPCT-11.2 constructed at the
 Roswell Park Cancer Institute by the group of Pieter de Jong. For
 further details see http://bacpac.med.buffalo.edu/
 VECTOR: pBACe3.6
 This sequence is the entire insert of clone RP11-404F10.

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 /clone_1lb="RPCT-11.2"
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 1321..1371
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 1571..1868
 /note="AluSc repeat: matches 1..228 of consensus"
 2888..3336
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 3518..3526
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repeat__region 4148..4451
/note="AluSx repeat: matches 1..301 of consensus"
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/note="LIM3 repeat: matches 5510..6077 of consensus"
repeat__region 5037..5064
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repeat__region 5065..5371
/note="AluSx repeat: matches 1..309 of consensus"
repeat__region 5372..5564
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/note="13 copies 4 mer gtcg 82% conserved"
repeat__region 5655..5696
/note="21 copies 2 mer tg 88% conserved"
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repeat__region 13099..13146
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repeat__region 23143..23315
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repeat__region 23891..24037
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/note="MIR repeat: matches 48..120 of consensus"
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/note="L2 repeat: matches 759..1644 of consensus"
repeat__region 26503..26800
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repeat__region 26801..27545
/note="L2 repeat: matches 1644..2710 of consensus"
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repeat__region 28716..28801
/note="43 copies 2 mer aa 65% conserved"
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/note="L2 repeat: matches 2411..2750 of consensus"
repeat__region 30905..31132
/note="LIM4 repeat: matches 6061..6289 of consensus"
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Query Match 33.7%; Score 910; DB 9; Length 195976;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1060; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 976 AGATGAAATCCCACTGCTCAGAGTCCAGACACACCAAGCTATTGGCTATG 1035
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DB 140378 AGATGAAATCCCACTGCTCAGATCCAGACACCAAGGCTATTGGCTATG 140437
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QY 1036 AGAATGTTATCTAGACAGAGTGCACTCCCTTAAGTCTTGCTCAAAAAACAATTC 1095
|||
DB 140438 AGAATGTTATCTAGACAGAGTGCACTCCCTTAAGTCTTGCTCAAAAAACAATTC 140497

QY 1096 TCGGCCCAAGAAACATCGAAGAAATTCATGATTGACTAGAAAATCAAGAGAA 1155
DB 140498 TCGGCCCAAGAAACATCGAAGAAATTCATGATTGACTAGAAAATCAAGAGAA 140557
QY 1156 TGAAGAAAGTGTGATCTTTTCCAGGATTAATCTCGATGCTTCTTTAGATTAAAG 1215
DB 140558 TGAAGAAAGTGTGATCTTTTCCAGGATTAATCTCGATGCTTCTTTAGATTAAAG 140617
QY 1216 TTGCTAATTCATCCACTGCTGAGAAATCTCTCAAAACCCAGAAAGTTTAATCACTTCAT 1275
DB 140618 TTGCTAATTCATCCACTGCTGAGAAATCTCTCAAAACCCAGAAAGTTTAATCACTTCAT 140677
QY 1276 CCCAAAAATGGGATTTGGAATGTCAGAAACCATTAATAAAGTCTTAAGAAATTCCTTA 1335
DB 140678 CCCAAAAATGGGATTTGGAATGTCAGAAACCATTAATAAAGTCTTAAGAAATTCCTTA 140737
QY 1336 TAGAAATGTAAATGCAAGTCAACATTTAATGACAGCTGTTGTAATTAATGATGCTC 1395
DB 140738 TAGAAATGTAAATGCAAGTCAACATTTAATGACAGCTGTTGTAATTAATGATGCTC 140797
QY 1396 CAGGTCAAGTGTCTGAGATTTCATTCATCCAGGGCTTGGATGTCAGGATTAACAAGA 1455
DB 140798 CAGGTCAAGTGTCTGAGATTTCATTCATCCAGGGCTTGGATGTCAGGATTAACAAGA 140857
QY 1456 GTCTTGTCTACAGAGAGGCAAGAACCAAAACAGACAGAACTCCAGCAGAAAGCAT 1515
DB 140858 GTCTTGTCTACAGAGAGGCAAGAACCAAAACAGACAGAACTCCAGCAGAAAGCAT 140917
QY 1516 GCACCTGACAAATAATGATGATTAATTTGCTCTATAAATGATGCTCCAGCAGATAGCT 1575
DB 140918 GCACCTGACAAATAATGATGATTAATTTGCTCTATAAATGATGCTCCAGCAGATAGCT 140977
QY 1576 GAGCTTACACTAATTTGTCAGAGCTGCTGCTGCTCCTCATGATAATTTGGCTCAAAATGAT 1635
DB 140978 GAGCTTACACTAATTTGTCAGAGCTGCTGCTGCTCCTCATGATAATTTGGCTCAAAATGAT 141037
QY 1636 GAACTACTTTTCATAGACAGTTGTAGCAGAGCTGACACAGATTTCCCAAGAGGCCAGATGT 1695
DB 141038 GAACTACTTTTCATAGACAGTTGTAGCAGAGCTGACACAGATTTCCCAAGAGGCCAGATGT 141097
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DB 141098 GGATCCACAGAGCTTGAAGGTCAAGAGTTCAAAAGATGAAGATCAGGGTGTGTCAGCAT 141157
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DB 141158 GTTTGGCAGATATATTAATGAGACACAGAAAGTGTGATGSCCAAGACAAAGACCTCC 141217
QY 1816 AGCCAGGCTTCAATTTATGACACTTGTCTGCAAAAAGAAAGTCTAGGTTTAAAGCTGTGC 1875
DB 141218 AGCCAGGCTTCAATTTATGACACTTGTCTGCAAAAAGAAAGTCTAGGTTTAAAGCTGTGC 141277
QY 1876 CAGAAACCATCCCAATTAAGAGACCGAGTCTGAAGTCACTTGTAAATCTAGTGAAGAG 1935
DB 141278 CAGAAACCATCCCAATTAAGAGACCGAGTCTGAAGTCACTTGTAAATCTAGTGAAGAG 141337
QY 1936 ACTTGAAGTCAAGAGTGAAGCTGTGTGGGACCGGGGGGAGTGGGTAATCTTTAAACCTT 1995
DB 141338 ACTTGAAGTCAAGAGTGAAGCTGTGTGGGACCGGGGGGAGTGGGTAATCTTTAAACCTT 141397
QY 1996 TAAAGATGCTTAATTTCAATCAATAGATTTTATTAAGAACTTA 2038
DB 141398 TAAAGATGCTTAATTTCAATCAATAGATTTTATTAAGAACTTA 141440

RESULT 22
AX405882
LOCUS AX405882 1128 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 297 from Patent WO0222660.
ACCESSION AX405882
VERSION AX405882.1 GI:21439203
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Tang, Y.T., Liu, C., Zhou, P., Asundi, V., Zhang, J., Zhao, Q.A., Ren, F.,
Xue, A.J., Yang, Y., Wehrman, T., and Drmanac, R.T.
TITLE Novel nucleic acids and polypeptides
JOURNAL Patent: WO 0222660-A 297 21-MAR-2002;
HYSEQ, INC. (US)
FEATURES
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ORIGIN
Query Match 30.0%; Score 811; DB 6; Length 1128;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GAAGTGGCTTCAATTCAGTGGCTGACTTCCAGAGACGAATATGCTGTTCCCAACATG 61
DB 48 GAAGTGGCTTCAATTCAGTGGCTGACTTCCAGAGACGAATATGCTGTTCCCAACATG 107
QY 62 CCTCACCCCTCATATATCTTTGGCAGCTCAAGGGTCAAGCCTCTGGAACCGGTAA 121
DB 108 CCTCACCCCTCATATATCTTTGGCAGCTCAAGGGTCAAGCCTCTGGAACCGGTAA 167
QY 122 AGAGCTGGTGGTTCGTTGGTGGGGCCGTGACTTTTCCCTTAAGTCCAAATGAAGA 181
DB 168 AGAGCTGGTGGTTCGTTGGTGGGGCCGTGACTTTTCCCTTAAGTCCAAATGAAGA 227
QY 182 AGTTGACTTATTTGTGCGACCTTCAACACACACCCCTCTTGTCACTATACGACAGAAG 241
DB 228 AGTTGACTTATTTGTGCGACCTTCAACACACACCCCTCTTGTCACTATACGACAGAAG 287
QY 242 GGGCAGTATATGAGCCCAAAATGTAATAGGAGAGTGAAGTCTCCAGATGAGG 301
DB 288 GGGCAGTATATGAGCCCAAAATGTAATAGGAGAGTGAAGTCTCCAGATGAGG 347
QY 302 CTACTCCCTGAAGCTGAGCAAACTGAAGAAGATGATCAGGATCTACTATGTTGGGAT 361
DB 348 CTACTCCCTGAAGCTGAGCAAACTGAAGAAGATGATCAGGATCTACTATGTTGGGAT 407
QY 362 ATACAGTCTATCTCAGAGAGCCCTTCACCCGAGATGCTGATGTCTTACAGAGA 421
DB 408 ATACAGTCTATCTCAGAGAGCCCTTCACCCGAGATGCTGATGTCTTACAGAGA 467
QY 422 CCGTCAAGCCCTTAAGTCAATGAGGTCTGAGAGCAATTAAGATGAGCACTGTGTGAC 481
DB 468 CCGTCAAGCCCTTAAGTCAATGAGGTCTGAGAGCAATTAAGATGAGCACTGTGTGAC 527
QY 482 CAATCTGACATGCTGATGAGACATGGGGAAGAGATGTAATTAATACCTGAAGCCCT 541
DB 528 CAATCTGACATGCTGATGAGACATGGGGAAGAGATGTAATTAATACCTGAAGCCCT 587
QY 542 GGGGCAAGAGCCCAAGATGCTCAATATGAGTCTTCCCAATCTCTCGAGAGATGGG 601
DB 588 GGGGCAAGAGCCCAAGATGCTCAATATGAGTCTTCCCAATCTCTCGAGAGATGGG 647
QY 602 AGAAGATGATATGACCTTCACTGCGTTGCGCAGAAACCTGTGACAGAAACTTCTCAAG 661

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Db 648 AGAAGATGATATGACCTTCATCTGCGTTGCGAGAAACCTGTGACAGAAATCTTTCAG 707
QY 662 CCCATCTCTTGCCAGAGAGCTCTGTGAAGTGTGCTGATGAGACCCAGATCTCCCATGTGT 721
Db 708 CCCATCTCTTGCCAGAGAGCTCTGTGAAGTGTGCTGATGAGACCCAGATCTCCCATGTGT 767
QY 722 CCTCTGTGTCTCTGTGTGTGCGCCCTCTCTGCTCACTCTCTTGTGTCTGAGGCTATTTCT 781
Db 768 CCTCTGTGTCTCTGTGTGTGCGCCCTCTCTGCTCACTCTCTTGTGTCTGAGGCTATTTCT 827
QY 782 TTGGTTTTCGAAGAGAGAGACAAAGAG 812
Db 828 TTGGTTTTCGAAGAGAGAGACAAAGAG 858

RESULT 23
HSA271869 1074 bp mRNA linear PRI 03-MAR-2000
LOCUS HSA271869 Homo sapiens mRNA for 19A24 protein (19A24 gene) .
DEFINITION AJ271869 AJ271869.1 GI:7161174
ACCESSION 19A24 gene.
VERSION 19A24 gene.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1
AUTHORS Murphy, J.J., Norton, J.D., Hobby, P. and Sutton, B.J.
TITLE An early response gene that encodes an immunoglobulin superfamily member with structural similarity to CD2
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1074)
REFERENCE Murphy, J.J.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-2000) Murphy J.J., Immunology Research Group, Division of Life Sciences, King's College London, 150 Stamford Street, London, SE1 8WA, UNITED KINGDOM
LOCATION/Qualifiers
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34..1020
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ORIGIN
Query Match 28.9%; Score 782; DB 9; Length 1074;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 782; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CAGAGAGCAATATGCTGTGTTCCCAACATGCTCAACCTCATCTATCTTTGGCAGC 90
Db 23 CAGAGAGCAATATGCTGTGTTCCCAACATGCTCAACCTCATCTATCTTTGGCAGC 82
QY 91 TCACAGGCTCAGACGCTCTGAGACCCGTGAAGAGCTGTGCTTCCGTTGGTGGGCGG 150
Db 83 TCACAGGCTCAGACGCTCTGAGACCCGTGAAGAGCTGTGCTTCCGTTGGTGGGCGG 142

QY 151 TGACTTTCCCCCTGAAGTCCAAAGTAAGCAAGTGAAGCTATATGTTGTCGACCTTCAACA 210
Db 143 TGACTTTCCCCCTGAAGTCCAAAGTAAGCAAGTGAAGCTATATGTTGTCGACCTTCAACA 202
QY 211 CAACCCCTTGTGTACCATATGAGCCAGAAAGGGGCACTATCATATGATGACCCAAATCGTA 270
Db 203 CAACCCCTTGTGTACCATATGAGCCAGAAAGGGGCACTATCATATGATGACCCAAATCGTA 262
QY 271 ATAGGAGAGATTAAGCTTCCAGATGAGAGGCTACTCCCTGAAAGCTCAGCAAACTGAAGA 330
Db 263 ATAGGAGAGATTAAGCTTCCAGATGAGAGGCTACTCCCTGAAAGCTCAGCAAACTGAAGA 322
QY 331 AGAATGACTCAGGAGTCTACTATGTGGGATATTAAGCTCATCTCCAGACCCCTCCA 390
Db 323 AGAATGACTCAGGAGTCTACTATGTGGGATATTAAGCTCATCTCCAGACCCCTCCA 382
QY 391 CCAGAGATGACGTGTGCTGATGTCTACGAGCACCTGTCAAAGCTTAAGTACCATGGTTC 450
Db 383 CCAGAGATGACGTGTGCTGATGTCTACGAGCACCTGTCAAAGCTTAAGTACCATGGTTC 442
QY 451 TGCAGAGCAATTAAGATGGCACTGTGTGACCAATCTGACATGTCATGGAACATGGGG 510
Db 443 TGCAGAGCAATTAAGATGGCACTGTGTGACCAATCTGACATGTCATGGAACATGGGG 502
QY 511 AAGAGATGTGATTTATACCTGGAAGGCCCTTGGGCAAGACCAATGATGTCCTTAATG 570
Db 503 AAGAGATGTGATTTATACCTGGAAGGCCCTTGGGCAAGACCAATGATGTCCTTAATG 562
QY 571 GGTTCATCTCTCCCATCTCTCTGAGATGGGAGAAAGTATGATGATCTTCATCTGCGTTG 630
Db 563 GGTTCATCTCTCCCATCTCTCTGAGATGGGAGAAAGTATGATGATCTTCATCTGCGTTG 622
QY 631 CCAGAACCTGTGCGAGAAACCTCTCAAGCCCATCTGCGAGAAAGCTCTGGAAG 690
Db 623 CCAGAACCTGTGCGAGAAACCTCTCAAGCCCATCTGCGAGAAAGCTCTGGAAG 682
QY 691 GTGCTGTGATGACCAAGATTCCTTCATGATGATGATGATGATGATGATGATGATGATGATG 750
Db 683 GTGCTGTGATGACCAAGATTCCTTCATGATGATGATGATGATGATGATGATGATGATGATG 742
QY 751 TGCTAGTCTCTTGTGATGCTGGGGCTATTTCTTGTGTTCTGAAGAGAGACAAGAAG 810
Db 743 TGCTAGTCTCTTGTGATGCTGGGGCTATTTCTTGTGTTCTGAAGAGAGACAAGAAG 802
QY 811 AG 812
Db 803 AG 804

RESULT 24
AR379856 921 bp DNA linear PAT 18-DEC-2003
LOCUS AR379856 Sequence 401 from patent US 6607879.
DEFINITION AR379856
ACCESSION AR379856
VERSION AR379856.1 GI:40087490
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 921)
AUTHORS Cocks, B.G., Stuart, S.G. and Seilhammer, J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 401 19-DEC-2003;
FEATURES
source Location/Qualifiers
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/organism="unknown"
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ORIGIN
Query Match 24.0%; Score 649; DB 6; Length 921;
Best Local Similarity 99.8%; Pred. No. 0;

[illegible]

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humaneXons or transcripts, for detecting expression and other uses
thereof
Patent: WO 02068579-A 4651 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
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ORIGIN

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					Gaps	
					0	
Qy	42	ATGCGTGGTTC	CCCAACATGCTC	CAACCTTCA	TATCTCTTGGCAGCTCA	CAAGGTCA 101
Db	1	ATGCGTGGTTC	CCCAACATGCTC	CAACCTTCA	TATCTCTTGGCAGCTCA	CAAGGTCA 60
Qy	102	GCAGCTTC	TGGACCCGTGA	AAAGCTGTGCGGTTCCGTTGGGGCCGTGA	CTTTCCCC 161	
Db	61	GCAGCTTC	TGGACCCGTGA	AAAGCTGTGCGGTTCCGTTGGGGCCGTGA	CTTTCCCC 120	
Qy	162	CTGAAGTCCAA	AGTAAAGCAAGTGA	CTCTATCTGTGGACCTTCA	ACAAACCCCTCTT 221	
Db	121	CTGAAGTCCAA	AGTAAAGCAAGTGA	CTCTATCTGTGGACCTTCA	ACAAACCCCTCTT 180	
Qy	222	GTCACCATTA	CAGCAGAAAGGGGGCACTATCA	TATGAGCCCAAAATCTG	TAATAGGAGAGA 281	
Db	181	GTCACCATTA	CAGCAGAAAGGGGGCACTATCA	TATGAGCCCAAAATCTG	TAATAGGAGAGA 240	
Qy	282	GTAGACTTCC	CAATGAGAGGCTACTCCCTGAAGCTCA	GACAACTGAAGAAATGATCA	341	
Db	241	GTAGACTTCC	CAATGAGAGGCTACTCCCTGAAGCTCA	GACAACTGAAGAAATGATCA	300	
Qy	342	GGGATCTA	CTATGTGGGGATTA	TACAGTCA	TCTCCAGAGCCCTCA	CAACCAAGATAC 401
Db	301	GGGATCTA	CTATGTGGGGATTA	TACAGTCA	TCTCCAGAGCCCTCA	CAACCAAGATAC 360
Qy	402	GTGCTGATG	CTATCGAGACCTGTCA	AAAGCTTAAAGTCA	ATGAGGCTGACAGCAAT 461	
Db	361	GTGCTGATG	CTATCGAGACCTGTCA	AAAGCTTAAAGTCA	ATGAGGCTGACAGCAAT 420	
Qy	462	AAGATGSCA	CTGTGTGACCACTGA	CACTGCTGATGAA	CAATGGGGAAGAGATGTG 521	
Db	421	AAGATGSCA	CTGTGTGACCACTGA	CACTGCTGATGAA	CAATGGGGAAGAGATGTG 480	
Qy	522	ATTATACT	TGAAGAGCCCTGGGGCAAGCCCA	TAGTAGTCCATTA	TGGTTCATCTCTC 581	
Db	481	ATTATACT	TGAAGAGCCCTGGGGCAAGCCCA	TAGTAGTCCATTA	TGGTTCATCTCTC 540	
Qy	582	CCCATCTTC	TGAGATGGGAGAAAGTAT	ATGACTTCA	TCTGCGTTGCCAGAAACCTT 641	
Db	541	CCCATCTTC	TGAGATGGGAGAAAGTAT	ATGACTTCA	TCTGCGTTGCCAGAAACCTT 600	
Qy	642	GTGAGCAAA	ACTTCTCAAGCCCATCTCTT	GCCAGAGAAAGCTCTGTAAG 690		
Db	601	GTGAGCAAA	ACTTCTCAAGCCCATCTCTT	GCCAGAGAAAGCTCTGTAAG 649		

RESULT	26
LOCUS	HSMB04336
DEFINITION	HSM804336
ACCESSION	Homosapiens mRNA; CDNA DKFZp666F188 (from clone DKFZp666F188).
VERSION	AL833025
KEYWORDS	AL833025.1 GI:21733615
SOURCE	.
ORGANISM	Homo sapiens (human)
	Homosapiens
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 1250)
AUTHORS	Anstoye,W., Witkner,U., Nemes,H.W., weil,B. and Wiemann,S.

TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp666F188) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further information about the clone and the sequencing project is available at <http://mips.gsf.de/proj/cDNA/>.
Location/Qualifiers
1. 1250
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="RZPD:DKFZp666F188"
/db_xref="taxon:9606"
/clone="DKFZp666F188"
/issue_type="stomach"
/clone_lib="666 (synonym: hsc02). Vector pSport1; host DH10B; sites NciI + SalI"
/dev_stage="adult"
1210..1215
polya_signal
polya_site
1239

Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1450 CCAAGAGCTTGTCTACAGAGAGGCAAGAACCAAAAGACAGACAGATCCAGAGAA 1509
1 CCAAGAGCTTGTCTACAGAGAGGCAAGAACCAAAAGACAGACAGATCCAGAGAA 60

1510 GCAGATGCACCTGACAAAATGATGATTAATGGCTCTATTAATATGTCGCCAGAC 1569
61 GCAGATGCACCTGACAAAATGATGATTAATGGCTCTATTAATATGTCGCCAGAC 120

1570 TATGCTGAGCTTACATTAATGTTGTCAGAGTGCTGCTGCCCCATGAAATGGCTCCA 1629
121 TATGCTGAGCTTACATTAATGTTGTCAGAGTGCTGCTGCCCCATGAAATGGCTCCA 180

1630 ATGAATGAATCTACTTTTCATGAGCAGTTGTAGACGCTGACACAGATTCGCCAGAGGCC 1689
181 ATGAATGAATCTACTTTTCATGAGCAGTTGTAGACGCTGACACAGATTCGCCAGAGGCC 240

1690 AGGTGTGATCCACAGAGCTTGAAGTCAAGTTCAAAAGATGAAGAATCAGGGTAGCT 1749
241 AGGTGTGATCCACAGAGCTTGAAGTCAAGTTCAAAAGATGAAGAATCAGGGTAGCT 300

1750 GACCATGTTGGCAGATCTATTAATGAGACACAGAAAGTGTCATGGCCCAAGAGCAAG 1809
301 GACCATGTTGGCAGATCTATTAATGAGACACAGAAAGTGTCATGGCCCAAGAGCAAG 360

1810 ACCCTCAGCAGGCTTCATTTATGCACTTGCTGCAAAAAGAAAGTCTAGGTTTAAG 1869
361 ACCCTCAGCAGGCTTCATTTATGCACTTGCTGCAAAAAGAAAGTCTAGGTTTAAG 420

1870 CTGTGCGAAGACCCATCCCAATTAAGACCCGAGCTGTAAGTCACTTGTAAATCTAGTG 1929
421 CTGTGCGAAGACCCATCCCAATTAAGACCCGAGCTGTAAGTCACTTGTAAATCTAGTG 480

1930 TGGAGACTTGGAGTGAAGCAGTGAAGTGGGGCAGGGGGGAGTGGGACTTGA 1989
481 TGGAGACTTGGAGTGAAGCAGTGAAGTGGGGCAGGGGGGAGTGGGACTTGA 540

1990 AACCTTTAAAGATGTTAATTCATTCATATAGATATTATTATTAAGACCTA 2038
541 AACCTTTAAAGATGTTAATTCATTCATATAGATATTATTATTAAGACCTA 589

RESULT 27

C0723314
LOCUS C0723314 1350 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 9248 from Patent WO02068579.
ACCESSION C0723314
VERSION C0723314.1 GI:42284171
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
Patent: WO 02068579-A 9248 06-SEP-2002;
PE Corporation (US)
FEATURES
source
1. 1350
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e-212;
Matches 376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

42 ATGGCTGTTTCCCAACATGCTCCTCATCTATATCTTTGGCAGCTCAGAGGTCA 101
1 ATGGCTGTTTCCCAACATGCTCCTCATCTATATCTTTGGCAGCTCAGAGGTCA 60

102 GCAGCCTTGACCCCGTGAAGAGAGTGGTCCGTTGGTGGGGCCGTGACTTCCC 161
61 GCAGCCTTGACCCCGTGAAGAGAGTGGTCCGTTGGTGGGGCCGTGACTTCCC 120

162 CTGAAGTCCAAAGTAAGCAAGTTGCTCTATTTGCTGAGCCTTCAACACACCCCTCT 221
121 CTGAAGTCCAAAGTAAGCAAGTTGCTCTATTTGCTGAGCCTTCAACACACCCCTCT 180

222 GTACCATATACAGCCGAAAGGGGGCACTATCATAGTACCCCAAAATCGTATATGGAGAGA 281
181 GTACCATATACAGCCGAAAGGGGGCACTATCATAGTACCCCAAAATCGTATATGGAGAGA 240

282 GTAGACTTCCAGATGAGAGGCTACTCCTGGAAGCTCAGCAAACTGAAAGATGATCA 341
241 GTAGACTTCCAGATGAGAGGCTACTCCTGGAAGCTCAGCAAACTGAAAGATGATCA 300

342 GGGATCTACTATGTGGGATATATACGCTCATCTCCAGAGCCCTCCAGGAGTAG 401
301 GGGATCTACTATGTGGGATATATACGCTCATCTCCAGAGCCCTCCAGGAGTAG 360

402 GTGCTGCATGTCTACG 417
361 GTGCTGCATGTCTACG 376

RESULT 28

C0071439
LOCUS C0071439 522 bp DNA linear PAT 20-JAN-2004
DEFINITION Sequence 7239 from Patent WO0157278.
ACCESSION C0071439
VERSION C0071439.1 GI:41041308
KEYWORDS
SOURCE Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human heia cells or other human cervical epithelialcells

JOURNAL Patent: WO 0157278-A 7239 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
Source 1..522
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL121985.13-EXPRESSED IN HELA, SIGNAL = 7.8"

ORIGIN
Query Match 11.9%; Score 323; DB 6; Length 522;
Best Local Similarity 100.0%; Pred. No. 3.3e-180;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 AGGCTCAGCAGCCTCTGGAGCCCGTGAAGAGCTGGTCCGTTCCGTTGGGGCCGCTGAC 154
DB 138 AGGCTCAGCAGCCTCTGGAGCCCGTGAAGAGCTGGTCCGTTCCGTTGGGGCCGCTGAC 197
QY 155 TTTCCCCCTGAAGTCCAAAGTAAGCAAGTTGACTATTTGCTGAGCCTTCAACACAAAC 214
DB 198 TTTCCCCCTGAAGTCCAAAGTAAGCAAGTTGACTATTTGCTGAGCCTTCAACACAAAC 257
QY 215 CCCTCTTGTACCATACAGCCAGAGGGGGCACTATCATATGAGCCCAAAATGTAATAG 274
DB 258 CCCTCTTGTACCATACAGCCAGAGGGGGCACTATCATATGAGCCCAAAATGTAATAG 317
QY 275 GGAAGAGTGAAGTCTCCCAAGTGAAGGCTTCTCCGTAAGCTCAGCAAACTGAAGAA 334
DB 318 GGAAGAGTGAAGTCTCCCAAGTGAAGGCTTCTCCGTAAGCTCAGCAAACTGAAGAA 377
QY 335 TGACTCAGGAGTCTATATGAGGGGATATACAGCTCATCTCCAGAGCCCTCCACCA 394
DB 378 TGACTCAGGAGTCTATATGAGGGGATATACAGCTCATCTCCAGAGCCCTCCACCA 437
QY 395 GGAGTACGTGCTGATGTCTACG 417
DB 438 GGAGTACGTGCTGATGTCTACG 460

RESULT 29
CO102023 522 bp DNA linear PAT 21-JAN-2004
LOCUS Sequence 10882 from Patent WO0157272.
DEFINITION CO102023
ACCESSION CO102023.1 GI:41071049
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
JOURNAL Patent: WO 0157272-A 10882 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
Source 1..522
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL121985.13-EXPRESSED IN PLACENTA, SIGNAL = 5.5"

ORIGIN
Query Match 11.9%; Score 323; DB 6; Length 522;
Best Local Similarity 100.0%; Pred. No. 3.3e-180;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 AGGCTCAGCAGCCTCTGGAGCCCGTGAAGAGCTGGTCCGTTCCGTTGGGGCCGCTGAC 154
DB 138 AGGCTCAGCAGCCTCTGGAGCCCGTGAAGAGCTGGTCCGTTCCGTTGGGGCCGCTGAC 197

QY 155 TTTCCCCCTGAAGTCCAAAGTAAGCAAGTTGACTATTTGCTGAGCCCTTCAACACAAAC 214
DB 198 TTTCCCCCTGAAGTCCAAAGTAAGCAAGTTGACTATTTGCTGAGCCCTTCAACACAAAC 257
QY 215 CCCTCTTGTACCATACAGCCAGAGGGGGCACTATCATATGAGCCCAAAATGTAATAG 274
DB 258 CCCTCTTGTACCATACAGCCAGAGGGGGCACTATCATATGAGCCCAAAATGTAATAG 317
QY 275 GGAAGAGTGAAGTCTCCCAAGTGAAGGCTTCTCCGTAAGCTCAGCAAACTGAAGAA 334
DB 318 GGAAGAGTGAAGTCTCCCAAGTGAAGGCTTCTCCGTAAGCTCAGCAAACTGAAGAA 377
QY 335 TGACTCAGGAGTCTATATGAGGGGATATACAGCTCATCTCCAGAGCCCTCCACCA 394
DB 378 TGACTCAGGAGTCTATATGAGGGGATATACAGCTCATCTCCAGAGCCCTCCACCA 437
QY 395 GGAGTACGTGCTGATGTCTACG 417
DB 438 GGAGTACGTGCTGATGTCTACG 460

RESULT 30
CO140985 522 bp DNA linear PAT 21-JAN-2004
LOCUS Sequence 11007 from Patent WO0157276.
DEFINITION CO140985
ACCESSION CO140985.1 GI:41098357
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157276-A 11007 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
Source 1..522
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL121985.13-EXPRESSED IN BONE MARROW, SIGNAL = 6.1"

ORIGIN
Query Match 11.9%; Score 323; DB 6; Length 522;
Best Local Similarity 100.0%; Pred. No. 3.3e-180;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 AGGCTCAGCAGCCTCTGGAGCCCGTGAAGAGCTGGTCCGTTCCGTTGGGGCCGCTGAC 154
DB 138 AGGCTCAGCAGCCTCTGGAGCCCGTGAAGAGCTGGTCCGTTCCGTTGGGGCCGCTGAC 197
QY 155 TTTCCCCCTGAAGTCCAAAGTAAGCAAGTTGACTATTTGCTGAGCCTTCAACACAAAC 214
DB 198 TTTCCCCCTGAAGTCCAAAGTAAGCAAGTTGACTATTTGCTGAGCCTTCAACACAAAC 257
QY 215 CCCTCTTGTACCATACAGCCAGAGGGGGCACTATCATATGAGCCCAAAATGTAATAG 274
DB 258 CCCTCTTGTACCATACAGCCAGAGGGGGCACTATCATATGAGCCCAAAATGTAATAG 317
QY 275 GGAAGAGTGAAGTCTCCCAAGTGAAGGCTTCTCCGTAAGCTCAGCAAACTGAAGAA 334
DB 318 GGAAGAGTGAAGTCTCCCAAGTGAAGGCTTCTCCGTAAGCTCAGCAAACTGAAGAA 377
QY 335 TGACTCAGGAGTCTATATGAGGGGATATACAGCTCATCTCCAGAGCCCTCCACCA 394
DB 378 TGACTCAGGAGTCTATATGAGGGGATATACAGCTCATCTCCAGAGCCCTCCACCA 437
QY 395 GGAGTACGTGCTGATGTCTACG 417
DB 438 GGAGTACGTGCTGATGTCTACG 460

Db 438 GGAGTACGTCGTCATGCTCTACG 460

RESULT 31

LOCUS CQ176644 522 bp DNA linear PAT 21-JAN-2004

DEFINITION Sequence 8040 from Patent WO0157274.

ACCESSION CQ176644

VERSION CQ176644.1 GI:41171383

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R. Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human heart

JOURNAL Patent: WO 0157274-A 8040 09-AUG-2001;

FEATURES

source location/Qualifiers

1..522

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

/note="MAP TO AL121985.13-EXPRESSED IN HEART, SIGNAL = 6.4"

ORIGIN

Query Match 11.9%; Score 323; DB 6; Length 522;

Best Local Similarity 100.0%; Pred. No. 3.3e-180;

Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 AGGGTCAGACGCTCTGGAACCGGTGAAGAGCTGTGGTCCGTTGGTGGGGCCGTGAC 154

Db 138 AGGGTCAGACGCTCTGGAACCGGTGAAGAGCTGTGGTCCGTTGGTGGGGCCGTGAC 197

QY 155 TTTCCCTGAAAGTCCAAAGTAAGCAAGTTGACTATTTGTTGACCTTCAACACAC 214

Db 198 TTTCCCTGAAAGTCCAAAGTAAGCAAGTTGACTATTTGTTGACCTTCAACACAC 257

QY 215 CCTCTTGTACCATACAGCAGAGGGGGCACTATCATATGACCCCAAAATCGTAATAG 274

Db 258 CCTCTTGTACCATACAGCAGAGGGGGCACTATCATATGACCCCAAAATCGTAATAG 317

QY 275 GGAGAGTACGTCCTCCAGATGAGAGGCTACTCCCTGAAGCTCAGCAACTGAAGAAGA 334

Db 318 GGAGAGTACGTCCTCCAGATGAGAGGCTACTCCCTGAAGCTCAGCAACTGAAGAAGA 377

QY 335 TGACTCAGGATCTACTATGTGGGATATACAGCTCATCTCCAGACCCCTCCACCA 394

Db 378 TGACTCAGGATCTACTATGTGGGATATACAGCTCATCTCCAGACCCCTCCACCA 437

QY 395 GGAGTACGTCGTCATGCTCTACG 417

Db 438 GGAGTACGTCGTCATGCTCTACG 460

RESULT 32

LOCUS CQ224251 522 bp DNA linear PAT 21-JAN-2004

DEFINITION Sequence 11090 from Patent WO0157273.

ACCESSION CQ224251

VERSION CQ224251.1 GI:41206669

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R. HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO

3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03 August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000 (03.10.00)<150> US 60/236,359<151> 27 September 2000 (27.09.00)<150> US 60/234,687<151> 21 September 2000 (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170> Molecular Dynamics Sequence Listing Engine

Patent: WO 0157273-A 11090 09-AUG-2001;

QY 95 AGGGTCAGACGCTCTGGAACCGGTGAAGAGCTGTGGTCCGTTGGTGGGGCCGTGAC 154

Db 138 AGGGTCAGACGCTCTGGAACCGGTGAAGAGCTGTGGTCCGTTGGTGGGGCCGTGAC 197

QY 155 TTTCCCTGAAAGTCCAAAGTAAGCAAGTTGACTATTTGTTGACCTTCAACACAC 214

Db 198 TTTCCCTGAAAGTCCAAAGTAAGCAAGTTGACTATTTGTTGACCTTCAACACAC 257

QY 215 CCTCTTGTACCATACAGCAGAGGGGGCACTATCATATGACCCCAAAATCGTAATAG 274

Db 258 CCTCTTGTACCATACAGCAGAGGGGGCACTATCATATGACCCCAAAATCGTAATAG 317

QY 275 GGAGAGTACGTCCTCCAGATGAGAGGCTACTCCCTGAAGCTCAGCAACTGAAGAAGA 334

Db 318 GGAGAGTACGTCCTCCAGATGAGAGGCTACTCCCTGAAGCTCAGCAACTGAAGAAGA 377

QY 335 TGACTCAGGATCTACTATGTGGGATATACAGCTCATCTCCAGACCCCTCCACCA 394

Db 378 TGACTCAGGATCTACTATGTGGGATATACAGCTCATCTCCAGACCCCTCCACCA 437

QY 395 GGAGTACGTCGTCATGCTCTACG 417

Db 438 GGAGTACGTCGTCATGCTCTACG 460

RESULT 33

LOCUS CQ262264 522 bp DNA linear PAT 23-JAN-2004

DEFINITION Sequence 10525 from Patent WO0157277.

ACCESSION CQ262264

VERSION CQ262264.1 GI:41234744

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R. Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver

JOURNAL Patent: WO 0157277-A 10525 09-AUG-2001;

FEATURES

source location/Qualifiers

1..522

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

/note="MAP TO AL121985.13-EXPRESSED IN FETAL LIVER, SIGNAL = 7.5"

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Query Match 11.9%; Score 323; DB 6; Length 522;
Best Local Similarity 100.0%; Pred. No. 3.3e-180; Indels 0; Gaps 0;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 AGGTCAGCAGCCTCTGGACCCGTTGAAAGAGCTGTCGGTTCGTTGGTGGGCGGTGAC 154
DB 138 AGGTCAGCAGCCTCTGGACCCGTTGAAAGAGCTGTCGGTTCGTTGGTGGGCGGTGAC 197
QY 155 TTTCCCTGTAAGTCCAAAGTAAGCAAGTGTATTTGTCTGGACCTTCAACACAC 214
DB 198 TTTCCCTGTAAGTCCAAAGTAAGCAAGTGTATTTGTCTGGACCTTCAACACAC 257
QY 215 CCCTCTTGTCACATACAGCCAGAGGGGCACTATCATAGTGACCCAAATCGTAATAG 274
DB 258 CCCTCTTGTCACATACAGCCAGAGGGGCACTATCATAGTGACCCAAATCGTAATAG 317
QY 275 GGAGAGTAAGTACTTCCAGATGGAGGCTACTCCCTGAAAGCTGACAACTGAAGAAG 334
DB 438 GGAGTAAGTACTTCCAGATGGAGGCTACTCCCTGAAAGCTGACAACTGAAGAAG 377

RESULT 34
LOCUS CO299336 522 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 10441 from Patent WO0186003.
ACCESSION CO299336
VERSION CO299336.1 GI:41259913
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human lung
JOURNAL Patent: WO 0186003-A 10441 15-NOV-2001;
Aeomica, Inc. (US)
FEATURES
Location/Qualifiers
1..522
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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/note="MAP TO AL121985.13-EXPRESSED IN LUNG, SIGNAL = 5.9"

ORIGIN
Query Match 11.9%; Score 323; DB 6; Length 522;
Best Local Similarity 100.0%; Pred. No. 3.3e-180; Indels 0; Gaps 0;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 AGGTCAGCAGCCTCTGGACCCGTTGAAAGAGCTGTCGGTTCGTTGGTGGGCGGTGAC 154
DB 138 AGGTCAGCAGCCTCTGGACCCGTTGAAAGAGCTGTCGGTTCGTTGGTGGGCGGTGAC 197
QY 155 TTTCCCTGTAAGTCCAAAGTAAGCAAGTGTATTTGTCTGGACCTTCAACACAC 214
DB 198 TTTCCCTGTAAGTCCAAAGTAAGCAAGTGTATTTGTCTGGACCTTCAACACAC 257
QY 215 CCCTCTTGTCACATACAGCCAGAGGGGCACTATCATAGTGACCCAAATCGTAATAG 274
DB 258 CCCTCTTGTCACATACAGCCAGAGGGGCACTATCATAGTGACCCAAATCGTAATAG 317
QY 275 GGAGAGTAAGTACTTCCAGATGGAGGCTACTCCCTGAAAGCTGACAACTGAAGAAG 334
DB 438 GGAGTAAGTACTTCCAGATGGAGGCTACTCCCTGAAAGCTGACAACTGAAGAAG 377

QY 335 TGACTCAGGATGTAATGTTGGGATATATACAGTCTATCAGAGCCCTCCACCCA 394
DB 378 TGACTCAGGATGTAATGTTGGGATATATACAGTCTATCAGAGCCCTCCACCCA 437

QY 395 GGAGTAAGTACTTCCAGATGGAGGCTACTCCCTGAAAGCTGACAACTGAAGAAG 417
DB 438 GGAGTAAGTACTTCCAGATGGAGGCTACTCCCTGAAAGCTGACAACTGAAGAAG 460

RESULT 35
LOCUS CO336448 522 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 10542 from Patent WO0157275.
ACCESSION CO336448
VERSION CO336448.1 GI:41285519
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human brain
JOURNAL Patent: WO 0157275-A 10542 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
Location/Qualifiers
1..522
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL121985.13-EXPRESSED IN BRAIN, SIGNAL = 7"

ORIGIN
Query Match 11.9%; Score 323; DB 6; Length 522;
Best Local Similarity 100.0%; Pred. No. 3.3e-180; Indels 0; Gaps 0;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 AGGTCAGCAGCCTCTGGACCCGTTGAAAGAGCTGTCGGTTCGTTGGTGGGCGGTGAC 154
DB 138 AGGTCAGCAGCCTCTGGACCCGTTGAAAGAGCTGTCGGTTCGTTGGTGGGCGGTGAC 197
QY 155 TTTCCCTGTAAGTCCAAAGTAAGCAAGTGTATTTGTCTGGACCTTCAACACAC 214
DB 198 TTTCCCTGTAAGTCCAAAGTAAGCAAGTGTATTTGTCTGGACCTTCAACACAC 257
QY 215 CCCTCTTGTCACATACAGCCAGAGGGGCACTATCATAGTGACCCAAATCGTAATAG 274
DB 258 CCCTCTTGTCACATACAGCCAGAGGGGCACTATCATAGTGACCCAAATCGTAATAG 317
QY 275 GGAGAGTAAGTACTTCCAGATGGAGGCTACTCCCTGAAAGCTGACAACTGAAGAAG 334
DB 318 GGAGTAAGTACTTCCAGATGGAGGCTACTCCCTGAAAGCTGACAACTGAAGAAG 377

QY 335 TGACTCAGGATGTAATGTTGGGATATATACAGTCTATCAGAGCCCTCCACCCA 394
DB 378 TGACTCAGGATGTAATGTTGGGATATATACAGTCTATCAGAGCCCTCCACCCA 437
QY 395 GGAGTAAGTACTTCCAGATGGAGGCTACTCCCTGAAAGCTGACAACTGAAGAAG 417
DB 438 GGAGTAAGTACTTCCAGATGGAGGCTACTCCCTGAAAGCTGACAACTGAAGAAG 460

RESULT 36
LOCUS AL159984 174215 bp DNA linear HTG 13-JUN-2001
DEFINITION Homo sapiens chromosome 17 clone RP11-167A1, 48 unordered pieces.
ACCESSION AL159984
VERSION AL159984.5 GI:9863577
KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL

1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Sims, S.
Direct Submission
Submitted (12-UN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Aug 21, 2000 this sequence version replaced gi:9230972.

----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: BA167A1
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 146348 bases at least Q40
Consensus quality: 156528 bases at least Q30
Consensus quality: 162553 bases at least Q20
Insert size: 169515; sum-of-contigs
Insert size: 156873; 10.5% error; agarose-fp
Quality coverage: 2.18x in Q20 bases; sum-of-contigs Quality
coverage: 3.50x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 48 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 3019: contig of 3019 bp in length
* 3020 3119: gap of 100 bp
* 3120 8692: contig of 5573 bp in length
* 8693 8792: gap of 100 bp
* 8793 12169: contig of 3377 bp in length
* 12170 12269: gap of 100 bp
* 12270 16502: contig of 4233 bp in length
* 16503 16602: gap of 100 bp
* 16603 21157: contig of 4555 bp in length
* 21158 21257: gap of 100 bp
* 21258 23365: contig of 2108 bp in length
* 23366 23465: gap of 100 bp
* 23466 25802: contig of 2337 bp in length
* 25803 25902: gap of 100 bp
* 25903 28533: contig of 2631 bp in length
* 28534 28633: gap of 100 bp
* 28634 35824: contig of 7191 bp in length
* 35825 35924: gap of 100 bp
* 35925 38376: contig of 2452 bp in length
* 38377 38476: gap of 100 bp
* 38477 47872: contig of 9396 bp in length
* 47873 47972: gap of 100 bp
* 47973 56612: contig of 8640 bp in length
* 56613 56712: gap of 100 bp
* 56713 59241: contig of 2529 bp in length
* 59242 59341: gap of 100 bp
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* 63224 63323: gap of 100 bp
* 63324 66069: contig of 2746 bp in length
* 66070 66169: gap of 100 bp
* 66170 68535: contig of 2366 bp in length
* 68536 68635: gap of 100 bp
* 68636 72163: contig of 3528 bp in length
* 72164 72263: gap of 100 bp
* 72264 75126: contig of 2863 bp in length
* 75127 75226: gap of 100 bp
* 75227 79331: contig of 4105 bp in length

* 79332 79431: gap of 100 bp
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* 84313 84412: gap of 100 bp
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* 88191 88290: gap of 100 bp
* 88291 92617: contig of 4337 bp in length
* 92618 92717: gap of 100 bp
* 92718 95401: contig of 2684 bp in length
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* 95502 97515: contig of 2014 bp in length
* 97516 97615: gap of 100 bp
* 97616 100727: contig of 3112 bp in length
* 100728 100827: gap of 100 bp
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* 113751 113850: gap of 100 bp
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* 115921 116020: gap of 100 bp
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* 118408 118507: gap of 100 bp
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* 152505 152604: gap of 100 bp
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* 155961 156060: gap of 100 bp
* 156061 163044: contig of 6984 bp in length
* 163045 163144: gap of 100 bp
* 163145 166969: contig of 3825 bp in length
* 166970 167069: gap of 100 bp
* 167070 169406: contig of 2337 bp in length
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8793. 12169

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VERSION
KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
Expressed sequence tags and encoded human proteins
Patent: EP 1033401-A 395 06-SEP-2000;
Genet (FR)
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Best Local Similarity 99.7%; Pred. No. 3.9e-155;
Matches 331; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 344)
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 388 02-OCT-2001;
GENSET

COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/388
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCCLAIR,JEAN YVES
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C1201/68//G06F17/30,C12N15/00,C12N5/00, PC
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FH Key Location/Qualifiers
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QY 1 GGAAGTGGCTTCAATTCAGTGGCTGACTTCCAGAGCAATATGGCTGGTCCCAACAT 60
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QY 61 GCCTCACCCCTCATCTATATCCTTTGGCAGCTCAAGGGTCAGCAGCCTTGCACCCGTGA 120
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DB 313 GCTACTCCCTGAAGCTCAGCAAACTGAAGAG 344

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LOCUS BD076035 347 bp DNA linear PAT 27-AUG-2002
DEFINITION 5' EST of secretory protein expressed in endoblast.
ACCESSION BD076035
VERSION BD076035.1 GI:22621638
KEYWORDS JP 2001512005-A/161.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 347)
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.

TITLE 5' EST of secretory protein expressed in endoblast
JOURNAL Patent: JP 2001512005-A 161 21-AUG-2001;
GENSET

COMMENT OS Homo sapiens (human)
PN JP 2001512005-A/161
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505194
PR 01-AUG-1997 US 08/904468
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCCLERT,BRUNO PI
LACROIX
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CC score 5.9
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Best Local Similarity 99.7%; Pred. No. 3.9e-155;
Matches 331; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 13 GGAAGTGGCTTCAATTCAGTGGCTGACTTCCAGAGCAATATGGCTGGTCCCAACAT 72
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QY 181 AAGTGAATCTATTTGTGTGACCTTCAACACAACCCCTCTTGTACGATACAGCCGAGAG 240
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DB 313 GCTACTCCCTGAAGCTCAGCAAACTGAAGAG 344

RESULT 40
LOCUS BD248091 401 bp DNA linear PAT 17-JUL-2003
DEFINITION 5' ESTs for secreted proteins expressed in various tissues.
ACCESSION BD248091
VERSION BD248091.1 GI:33057861
KEYWORDS JP 2002525024-A/156.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 401)
 AUTHORS Edwards,J.B.D.M., Duclerc,A. and Lacroix,B.
 TITLE 5' ESTs for secreted proteins expressed in various tissues
 JOURNAL Patent: JP 2002525024-A 156 13-AUG-2002;
 GENSER
 COMMENT OS Homo sapiens (human)
 FN JP 2002525024-A/156
 PD 13-AUG-2002
 PF 31-JUL-1998 JP 2000505294
 PR 01-AUG-1997 US 08/905051
 PI JEAN BAPTISTE DUMAS MILNE EDWARDS,ALYMERIC DUCLERC,BRUNO PI
 LACROIX
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 CC score 5.9
 CC seq LIIYLWLTGSA/SG
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 Oy 193 TTGCTGACCTTCAACACAAACCCCTCTGTGACCATATACAGCCGAAAGGGGGCACTATCA 252
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 Oy 253 TAGTGACCCAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGGCTACTCCCTGA 312
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Oy 313 AGCTCAGCAAACTGAAGAAGATGACTCAG 342
 Db 301 AGCTCAGCAAACTGAAGAAGATGACTCAG 330
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 LOCUS CQ772054 401 bp DNA linear PAT 04-MAR-2004
 DEFINITION Sequence 162 from Patent EP1375514.
 ACCESSION CQ772054
 VERSION CQ772054.1 GI:45126015
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Dumas Milne Edwards,J.B., Duclerc,A. and Lacroix,B.
 TITLE 5'ESTs for secreted proteins expressed in various tissues
 JOURNAL Patent: EP 1375514-A 162 02-JAN-2004;
 GENSER (FR)
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 Db 301 AGCTCAGCAAACTGAAGAAGATGACTCAG 330
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 DEFINITION Sequence 16459 from Patent WO0157278.
 ACCESSION CQ080659
 VERSION CQ080659.1 GI:41050528
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1

CO186535
LOCUS CO186535 275 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 17931 from Patent WO0157274.
ACCESSION CO186535
VERSION CO186535.1 GI:41181549
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human heart
JOURNAL Patent: WO 0157274-A 17931 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
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QY 203 CTTCACACAAACCCCTTTGTCTACCATACAGCCAGAGGGGACATATCATAGTACCA 262
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QY 263 AAATCGTAATAGGAGAGATGAGCTTCCAGATGAGGGCTACTCCCTGAAGCTCAGCA 322
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QY 323 ACTGAAGAGATGACTCAGGGATCTACTATGTGGGATATACGCTCATCTCAGCA 382
DB 181 ACTGAAGAGATGACTCAGGGATCTACTATGTGGGATATACGCTCATCTCAGCA 240
QY 383 GCCCTCCAGCAGAGTAGCTGTGCTGATGCTACG 417
DB 241 GCCCTCCAGCAGAGTAGCTGTGCTGATGCTACG 275
RESULT 46
LOCUS CO237182 275 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 24021 from Patent WO0157273.
ACCESSION CO237182
VERSION CO237182.1 GI:41220462
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO 3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03 August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000 (03.10.00)<150> US 60/236,359<151> 27 September 2000 (27.09.00)<150> US 60/234,687<151> 21 September 2000 (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170> Molecular Dynamics Sequence Listing Engine

JOURNAL Patent: WO 0157273-A 24021 09-AUG-2001;
Aeomica, Inc. (US)
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QY 323 ACTGAAGAGATGACTCAGGGATCTACTATGTGGGATATACGCTCATCTCAGCA 382
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QY 383 GCCCTCCAGCAGAGTAGCTGTGCTGATGCTACG 417
DB 241 GCCCTCCAGCAGAGTAGCTGTGCTGATGCTACG 275
RESULT 47
LOCUS CO274801 275 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 23062 from Patent WO0157277.
ACCESSION CO274801
VERSION CO274801.1 GI:41247405
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver
JOURNAL Patent: WO 0157277-A 23062 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
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QY 263 AATTCGTATATAGGAGAGAGATAGACTTCCCAAGTGAAGGCTACTCCCTGAAGCTCAGCA 322
Db 121 AATTCGTATATAGGAGAGAGATAGACTTCCCAAGTGAAGGCTACTCCCTGAAGCTCAGCA 180
QY 323 ACTGAAGAAGATGACTCAGGAGATCTACTATGAGGGGATATACAGCTCATCTCCAGCA 382
Db 181 ACTGAAGAAGATGACTCAGGAGATCTACTATGAGGGGATATACAGCTCATCTCCAGCA 240
QY 383 GCCCTCCACCAGAGAGTACGTGCTGATGCTAG 417
Db 241 GCCCTCCACCAGAGAGTACGTGCTGATGCTAG 275

RESULT 48
CQ311787 275 bp DNA linear PAT 23-JAN-2004
LOCUS CQ311787
DEFINITION Sequence 22892 from Patent WO0186003.
ACCESSION CQ311787
VERSION CQ311787.1 GI:41272364
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human lung
JOURNAL Patent: WO 0186003-A 22892 15-NOV-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..275
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL121985.13-EXPRESSED IN LUNG, SIGNAL =
5.9-NT HIT: AJ271869.1, EVALUE 0.00e+00-EST_HUMAN HIT:
AM963563.1, EVALUE 0.00e+00"

ORIGIN
Query Match 10.2%; Score 275; DB 6; Length 275;
Best Local Similarity 100.0%; Pred. No. 1.5e-151;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TGGGGCCGTGACTTTCCCTGAACTCAAGTAAAGCAAGTGAAGTGTGCTGAGC 202
Db 1 TGGGGCCGTGACTTTCCCTGAACTCAAGTAAAGCAAGTGAAGTGTGCTGAGC 60
QY 203 CTTCAACACACCCCTTGTGTCACATFACAGCCAGAGGGGGCAGCTATCATCTCCAGCA 262
Db 61 CTTCAACACACCCCTTGTGTCACATFACAGCCAGAGGGGGCAGCTATCATCTCCAGCA 120
QY 263 AATTCGTATATAGGAGAGAGATAGACTTCCCAAGTGAAGGCTACTCCCTGAAGCTCAGCA 322
Db 121 AATTCGTATATAGGAGAGAGATAGACTTCCCAAGTGAAGGCTACTCCCTGAAGCTCAGCA 180
QY 323 ACTGAAGAAGATGACTCAGGAGATCTACTATGAGGGGATATACAGCTCATCTCCAGCA 382
Db 181 ACTGAAGAAGATGACTCAGGAGATCTACTATGAGGGGATATACAGCTCATCTCCAGCA 240
QY 383 GCCCTCCACCAGAGAGTACGTGCTGATGCTAG 417
Db 241 GCCCTCCACCAGAGAGTACGTGCTGATGCTAG 275

RESULT 49
CQ349144 275 bp DNA linear PAT 23-JAN-2004
LOCUS CQ349144
DEFINITION Sequence 23238 from Patent WO0157275.
ACCESSION CQ349144

VERSION CQ349144.1 GI:41298215
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human brain
JOURNAL Patent: WO 0157275-A 23238 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..275
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/note="MAP TO AL121985.13-EXPRESSED IN BRAIN, SIGNAL =
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AM963563.1, EVALUE 0.00e+00"

ORIGIN
Query Match 10.2%; Score 275; DB 6; Length 275;
Best Local Similarity 100.0%; Pred. No. 1.5e-151;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TGGGGCCGTGACTTTCCCTGAACTCAAGTAAAGCAAGTGAAGTGTGCTGAGC 202
Db 1 TGGGGCCGTGACTTTCCCTGAACTCAAGTAAAGCAAGTGAAGTGTGCTGAGC 60
QY 203 CTTCAACACACCCCTTGTGTCACATFACAGCCAGAGGGGGCAGCTATCATCTCCAGCA 262
Db 61 CTTCAACACACCCCTTGTGTCACATFACAGCCAGAGGGGGCAGCTATCATCTCCAGCA 120
QY 263 AATTCGTATATAGGAGAGAGATAGACTTCCCAAGTGAAGGCTACTCCCTGAAGCTCAGCA 322
Db 121 AATTCGTATATAGGAGAGAGATAGACTTCCCAAGTGAAGGCTACTCCCTGAAGCTCAGCA 180
QY 323 ACTGAAGAAGATGACTCAGGAGATCTACTATGAGGGGATATACAGCTCATCTCCAGCA 382
Db 181 ACTGAAGAAGATGACTCAGGAGATCTACTATGAGGGGATATACAGCTCATCTCCAGCA 240
QY 383 GCCCTCCACCAGAGAGTACGTGCTGATGCTAG 417
Db 241 GCCCTCCACCAGAGAGTACGTGCTGATGCTAG 275

RESULT 50
AX905449 435 bp DNA linear PAT 18-DEC-2003
LOCUS AX905449
DEFINITION Sequence 21312 from Patent EP1033401.
ACCESSION AX905449
VERSION AX905449.1 GI:40060406
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Dumas Milne Edwards, J.B., Duclet, A. and Giordano, J.Y.
AUTHORS Expressed sequence tags and encoded human proteins
TITLE Patent: EP 1033401-A 21312 06-SEP-2000;
JOURNAL Genet (FR)
FEATURES
source Location/Qualifiers
1..435
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 6.7%; Score 182; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 5e-96;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1857 CTAGGTTTAAAGGCTGTCAGAACCCATCCCAATAAAGAGACCGAGCTGTAAGTCACAT 1916
 DB 1 CTAGGTTTAAAGGCTGTCAGAACCCATCCCAATAAAGAGACCGAGCTGTAAGTCACAT 60
 QY 1917 TGTAAATCTAGTAGAGAGACTTGAGCTCAGGACGAGTGTGGGGACCGGGGGCA 1976
 DB 61 TGTAAATCTAGTAGAGAGACTTGAGCTCAGGACGAGTGTGGGGACCGGGGGCA 120
 QY 1977 GTGGGTACTGTAAACCTTTAAAGATGTTTAATTCATTCAATGATATTTATTAAAGACC 2036
 DB 121 GTGGGTACTGTAAACCTTTAAAGATGTTTAATTCATTCAATGATATTTATTAAAGACC 180
 QY 2037 TA 2038
 DB 181 TA 182

RESULT 51
 BD040982
 LOCUS BD040982 435 bp DNA linear PAT 27-AUG-2002
 DEFINITION Sequence tag and encoded human protein.
 ACCESSION BD040982 GI:22582724
 VERSION BD040982.1 GI:22582724
 KEYWORDS JP 2001269182-A/17228.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 435)
 Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
 Sequence tag and encoded human protein
 Patent: JP 2001269182-A 17228 02-OCT-2001;
 GENSET

COMMENT
 OS Homo sapiens (human)
 PN JP 2001269182-A/17228
 PD 02-OCT-2001
 PE 24-FEB-2000 US 2000118773
 PR 26-FEB-1999 JP 60/122487
 PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
 PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
 C12N5/10,
 PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
 G06F15/40
 CC
 FH Key Location/Qualifiers.
 source 1.435 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN
 Query Match 6.7%; Score 182; DB 6; Length 435;
 Best Local Similarity 100.0%; Pred. No. 5e-96;
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 52
 CQ432314
 LOCUS CQ432314 392 bp DNA linear PAT 28-JAN-2004
 DEFINITION Sequence 17348 from Patent WO0151628.
 ACCESSION CQ432314
 VERSION CQ432314.1 GI:41384543
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1
 Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
 Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer
 Patent: WO 0151628-A 17348 19-JUL-2001;
 Millennium Pharmaceuticals, Inc. (US)

REFERENCE
 AUTHORS Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
 TITLE Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer
 JOURNAL Patent: WO 0151628-A 17348 19-JUL-2001;
 KEYWORDS Millennium Pharmaceuticals, Inc. (US)
 FEATURES
 source 1.392 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
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 Best Local Similarity 99.5%; Pred. No. 1.8e-89;
 Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1656 TGTAGCAGGCTGACACAGATTCACAGAGGGCCAGGTGTGATCCACAGACTTGAAG 1715
 DB 36 TGTAGCAGGCTGACACAGATTCACAGAGGGCCAGGTGTGATCCACAGACTTGAAG 95
 QY 1716 TCAAGTTCACAAAGATGAAGATCAGGCTGACATGTTGGCAGATTAATATG 1775
 DB 96 TCAAGTTCACAAAGATGAAGATCAGGCTGACATGTTGGCAGATTAATATG 155
 QY 1776 GAGACACAGAGTGTGATGCGCCAGACAGACCTCCAGCAGCTTCATTATGCA 1835
 DB 156 GAGACACAGAGTGTGATGCGCCAGACAGACCTCCAGCAGCTTCATTATGCA 215
 QY 1836 CTGTGCTGCAAAAAGAAAGTCTAGGTTTAAAGGCTGTGCA 1877
 DB 216 CTGTGCTGCAAAAAGAAAGTCTAGGTTTAAAGGCTGTGCA 257

RESULT 53
 CQ423465
 LOCUS CQ423465 329 bp DNA linear PAT 28-JAN-2004
 DEFINITION Sequence 8499 from Patent WO0151628.
 ACCESSION CQ423465
 VERSION CQ423465.1 GI:41375694
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1
 Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
 Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer
 Patent: WO 0151628-A 8499 19-JUL-2001;
 Millennium Pharmaceuticals, Inc. (US)

REFERENCE
 AUTHORS Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
 TITLE Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer
 JOURNAL Patent: WO 0151628-A 8499 19-JUL-2001;
 KEYWORDS Millennium Pharmaceuticals, Inc. (US)
 FEATURES
 source 1.329 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Query Match 4.8%; Score 129; DB 6; Length 329;
 Best Local Similarity 100.0%; Pred. No. 2.2e-64;

Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1656 TGTAGAGGCGCTGACCAAGATTCCAGAGGGCCAGGTGATTCACAGGATTGAAG 1715
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 Db 90 TGTAGAGGCGCTGACCAAGATTCCAGAGGGCCAGGTGATTCACAGGATTGAAG 149
 |||
 QY 1716 TCAAGCTCAAAAGATGAAGATCATGCGGTAGCTGACCATGTTGGCAGTACTATNAG 1775
 |||
 Db 150 TCAAGCTCAAAAGATGAAGATCATGCGGTAGCTGACCATGTTGGCAGTACTATNAG 209
 |||
 QY 1776 GAGACACAG 1784
 |||
 Db 210 GAGACACAG 218

RESULT 54
 AC013435/C AC013435 116283 bp DNA linear PRI 21-FEB-2002
 LOCUS
 DEFINITION Homo sapiens BAC clone RP11-52C8 from 2, complete sequence.
 AC013435
 VERSION AC013435.7 GI:18140107
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Sultston,J.R. and Waterston,R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 9847074
 PUBMED
 REFERENCE
 AUTHORS 2 (bases 1 to 116283)
 TITLE Tomlinson,C., Kozlowski,A. and Spalding,L.
 JOURNAL The sequence of Homo sapiens BAC clone RP11-52C8
 UNPUBLISHED (2001)
 REFERENCE
 AUTHORS 3 (bases 1 to 116283)
 TITLE Waterston,R.H.
 JOURNAL Direct Submision
 UNPUBLISHED (11-NOV-1999) Genome Sequencing Center, Washington
 UNIVERSITY School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE
 AUTHORS 4 (bases 1 to 116283)
 TITLE Waterston,R.H.
 JOURNAL Direct Submision
 UNPUBLISHED (13-JAN-2002) Genome Sequencing Center, Washington
 UNIVERSITY School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE
 AUTHORS 5 (bases 1 to 116283)
 TITLE Waterston,R.
 JOURNAL Direct Submision
 UNPUBLISHED (21-FEB-2002) Department of Genetics, Washington
 UNIVERSITY, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 ON Jan 13, 2002 this sequence version replaced gi:17647042.

COMMENT
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@wustl.wustl.edu
 ----- Summary Statistics
 Center Project name: H_NH0052C08

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence

from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPc1-11 human BAC library was made from the blood of one male donor, as described by Osogawa,K., Moon,P.Y., Zhao,B., Frengen,E., Tateo,M., Catanesse,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.choiri.org>
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-690121, 2000 bp overlap. Actual end of this clone is at base position 116283 of RP11-52C8.

FEATURES

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repeat_region	1..116283
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	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/chromosome="2"
	/map="2"
	/clone="RP11-52C8"
	/clone_11b="RPc1-11"
repeat_region	3..301
	/rpt_family="Alu"
repeat_region	446..478
	/rpt_family="(TG)n"
repeat_region	862..1291
	/rpt_family="n1"
repeat_region	1286..1321
	/rpt_family="AT-rich"
repeat_region	1301..1604
	/rpt_family="Alu"
repeat_region	1613..1904
	/rpt_family="Alu"
repeat_region	2072..2115
	/rpt_family="MIR"
repeat_region	2122..2209
	/rpt_family="MIR"
repeat_region	3549..3654
	/rpt_family="Alu"
repeat_region	3656..3921
	/rpt_family="Alu"
repeat_region	4042..4204
	/rpt_family="MIR"
repeat_region	4212..4246
	/rpt_family="MALR"
repeat_region	4320..4592
	/rpt_family="MER2_type"
repeat_region	4567..4592
	/rpt_family="AT-rich"
repeat_region	4593..4883
	/rpt_family="Alu"
repeat_region	4884..5139
	/rpt_family="MER2_type"
repeat_region	5140..5319
	/rpt_family="Alu"
repeat_region	5309..5347
	/rpt_family="(T)n"
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	/rpt_family="Alu"
repeat_region	5497..5789
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repeat_region	5790..5934
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repeat_region      6071. .6267
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repeat_region      6638. .6689
                    /rpt_family="MIR"
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                    /rpt_family="Alu"
repeat_region      7450. .7748
                    /rpt_family="Alu"
repeat_region      8170. .8263
                    /rpt_family="MaLR"
repeat_region      8438. .8682
                    /rpt_family="MaLR"
repeat_region      8689. .9295
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repeat_region      9934. .9995
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repeat_region      9996. .10287
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repeat_region      10284. .10320
                    /rpt_family="AT_rich"
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                    /rpt_family="L1"
repeat_region      10554. .10811
                    /rpt_family="Alu"
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                    /rpt_family="L1"
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                    /rpt_family="L1"
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                    /rpt_family="Alu"
repeat_region      14578. .14882
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repeat_region      15349. .15492
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repeat_region      15492. .15536
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repeat_region      16598. .16620
                    /rpt_family="AT_rich"
repeat_region      16768. .16800
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repeat_region      17497. .17590

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Query Match 2.8%; Score 76; DB 9; Length 116283;

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Best Local Similarity 100.0%; Pred. No. 1,le-32;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2066 CCTGTATCCACACTTTGGAGGCCAGTGGGTGATCTGATGATCAGACTTCA 2125
Db      68814 CCTGTATCCACACTTTGGAGGCCAGTGGGTGATCTGATGATCAGACTTCA 68755

Qy      2126 AGACGAGCTTGCCAA 2141
Db      68754 AGACGAGCTTGCCAA 68739

RESULT 55
LOCUS AC068218
DEFINITION Homo sapiens chromosome 2 clone RP11-105A13 map 2, *** SEQUENCING
IN PROGRESS ***, 32 unordered pieces.
ACCESSION AC068218
VERSION AC068218.2 GI:10280755
KEYWORDS HTG; HTGS PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 117432)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 117432)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Baetsen,V., Beda,F.,
Boguslavskiy,L., Boukhalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castelle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heatford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Lacroque,K., Lamazares,R., Landers,T., Lenocky,J.,
Levine,R., Lien,C., Liu,G., Locke,K., MacDonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPherson,R.,
Meldrum,J., Meneau,L., Mihova,T., Miranda,C., Miñana,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Pisani,C., Poltara,T.M., Oliver,J., Peterson,K., Pierre,N.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessfaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 23, 2000 this sequence version replaced gi:7671278.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green,P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seg.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10125
Center clone name: 105_A_13
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

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* be preserved.
* 1 637: contig of 637 bp in length
* 638 737: gap of 100 bp
* 738 1740: contig of 1003 bp in length
* 1741 1840: gap of 100 bp
* 1841 3127: contig of 1287 bp in length
* 3128 3227: gap of 100 bp
* 3228 4542: contig of 1315 bp in length
* 4543 4642: gap of 100 bp
* 4643 6297: contig of 1655 bp in length
* 6298 6397: gap of 100 bp
* 6398 8080: contig of 1683 bp in length
* 8081 8180: gap of 100 bp
* 8181 10438: contig of 2258 bp in length
* 10439 10538: gap of 100 bp
* 10539 12439: contig of 1901 bp in length
* 12440 12539: gap of 100 bp
* 12540 15004: contig of 2465 bp in length
* 15005 15104: gap of 100 bp
* 15105 17541: contig of 2437 bp in length
* 17542 19304: contig of 1663 bp in length
* 19305 19404: gap of 100 bp
* 19405 21237: contig of 1833 bp in length
* 21238 21337: gap of 100 bp
* 21338 22932: contig of 1595 bp in length
* 22933 23032: gap of 100 bp
* 23033 24746: contig of 1714 bp in length
* 24747 24846: gap of 100 bp
* 24847 27215: contig of 2369 bp in length
* 27216 27315: gap of 100 bp
* 27316 29028: contig of 1713 bp in length
* 29029 29128: gap of 100 bp
* 29129 30602: contig of 1474 bp in length
* 30603 30702: gap of 100 bp
* 30703 34245: contig of 3543 bp in length
* 34246 34345: gap of 100 bp
* 34346 36988: contig of 2643 bp in length
* 36989 37088: gap of 100 bp
* 37089 40052: contig of 2964 bp in length
* 40053 40152: gap of 100 bp
* 40153 43222: contig of 3070 bp in length
* 43223 43322: gap of 100 bp
* 43323 47009: contig of 3686 bp in length
* 47009 47108: gap of 100 bp
* 47109 50280: contig of 3172 bp in length
* 50281 50380: gap of 100 bp
* 50381 55078: contig of 4698 bp in length
* 55079 55178: gap of 100 bp
* 55179 60366: contig of 5188 bp in length
* 60367 60466: gap of 100 bp
* 60467 63933: contig of 3467 bp in length
* 63934 64033: gap of 100 bp
* 64034 68186: contig of 4153 bp in length
* 68187 68286: gap of 100 bp
* 68287 73579: contig of 5293 bp in length
* 73580 73679: gap of 100 bp
* 73680 80613: contig of 6934 bp in length
* 80614 80713: gap of 100 bp
* 80714 99197: contig of 18464 bp in length
* 99198 99297: gap of 100 bp
* 99298 108271: contig of 8974 bp in length
* 108272 108371: gap of 100 bp
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/db_xref="taxon:9606"
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/map="2"
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Best Local Similarity 100.0%; Pred. No. 1,1e-32;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2066 CCTGTATCCAGCACTTTGGAGGCCAGGTGGTGCATCTGAGTCAGAGTTCA 2125
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 Db 8768 CCTGTATCCAGCACTTTGGAGGCCAGGTGGTGCATCTGAGTCAGAGTTCA 8827
 |||||
 OY 2126 AGACGACCTGGCCAA 2141
 |||||
 Db 8828 AGACGACCTGGCCAA 8843
 |||||
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 AC023445/c
 LOCUS
 DEFINITION Homo sapiens chromosome 5 clone RP11-715K1 map 5, LOW-PASS SEQUENCE
 SAMPLING
 AC023445 156886 bp DNA linear HTG 11-APR-2000
 AC023445.2 GI:7533994
 HTG: HTGS PHASED.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 156886)
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 Homo sapiens chromosome 5, clone RP11-715K1
 Unpublished
 2 (bases 1 to 156886)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, U., Barna, N., Bede, F., Boguslavsky, L.,
 Boukhalter, B., Brown, A., Burkett, G., Campolano, A., Castle, A.,
 Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
 D'Arrellano, K., Dewar, K., Dodge, S., Domoni, M., Doyle, M.,
 Fenebor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D.,
 Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
 Grand, P., Grant, G., Hagos, B., Heath, A., Horton, L.,
 Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karas, A.,
 Klein, J., Landers, T., Largocque, K., Lehoczy, J., Levine, R.,
 Liu, C., Liu, G., Locke, K., McDonald, P., Margulis, N., McCarthy, M.,
 McEwan, P., McGurk, A., McKernan, K., McPherson, R., Meldrum, J.,
 Menon, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Naylor, J.,
 Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T. M.,
 Peterson, K., Piere, N., Pisan, C., Pollara, V., Raymond, C.,
 Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
 Sever, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Subramanian, A., Talama, J., Tesfaye, S., Theodore, J., Tirrell, A.,
 Travers, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,
 Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and
 Zody, M.
 Direct Submission
 Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 11, 2000 this sequence version replaced gi:6970665.
 All repeats were identified using RepeatMasker:
 Smit, A. F. A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: W1BR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submission@genome.wi.mit.edu
 ----- Project Information
 Center project name: L6374
 Center clone name: 715_K_1

 * NOTE: This record contains 173 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will

* be preserved.
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 778 777: contig of 777 bp in length
 878 877: gap of 100 bp
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 1759 1759: gap of 100 bp
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 4344 4344: gap of 100 bp
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 6233 6233: contig of 809 bp in length
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 7142 7142: gap of 100 bp
 7948 7948: contig of 806 bp in length
 8048 8048: gap of 100 bp
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 16123 16123: gap of 100 bp
 16933 16933: contig of 810 bp in length
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 21397 21397: contig of 791 bp in length
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 22298 22298: contig of 801 bp in length
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 23066 23066: contig of 668 bp in length
 23166 23166: gap of 100 bp
 23971 23971: contig of 805 bp in length
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 30237 30237: contig of 816 bp in length
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* 33929 34736: contig of 808 bp in length
* 34737 34836: gap of 100 bp
* 34837 35635: contig of 799 bp in length
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* 40969 41068: gap of 100 bp
* 41069 41877: contig of 809 bp in length
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* 43810 44588: contig of 779 bp in length
* 44589 44688: gap of 100 bp
* 44689 45484: contig of 796 bp in length
* 45485 45584: gap of 100 bp
* 45585 46387: contig of 802 bp in length
* 46387 46487: gap of 100 bp
* 46487 47279: contig of 792 bp in length
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* 47379 48314: contig of 836 bp in length
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* 49213 50013: contig of 801 bp in length
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* 52831 53644: contig of 814 bp in length
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* 54631 55431: contig of 801 bp in length
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* 55532 56309: contig of 778 bp in length
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* 58082 58181: gap of 100 bp
* 58182 58877: contig of 696 bp in length
* 58878 58977: gap of 100 bp
* 58978 59784: contig of 807 bp in length
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* 60688 60787: gap of 100 bp
* 60788 61588: contig of 801 bp in length
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QY 2103 GGTCACTGAGTCAAGAGTTCAAGACCAAGCTGGCCAAACATGTAAGAAACCCATCTCTA 2162
DB 15945 GGTCACTGAGTCAAGAGTTCAAGACCAAGCTGGCCAAACATGTAAGAAACCCATCTCTA 15886

QY 2163 CTAAGAT 2170
DB 15885 CTAAGAT 15878

RESULT 57
AC010598
LOCUS AC010598 174551 bp DNA linear PRI 22-MAR-2003
DEFINITION Homo sapiens chromosome 5 clone CTC-56009, complete sequence.
AC010598
ACCESSION AC010598
VERSION AC010598.6 GI:9558579
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 174551)
TITLE Direct Submission
JOURNAL Direct Submission
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (16-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT
On Jul 28, 2000 this sequence version replaced gi:7711473.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu

Quality: Phrap Quality >=40 99.4% of Sequence;
Estimated Total Number of Errors is 2.1.
STS Content:
WI-9707 G22840.

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QY 2103 GGTCACTGAGTCAAGAGTTCAAGACCAAGCTGGCCAAACATGTAAGAAACCCATCTCTA 2162
DB 134800 GGTCACTGAGTCAAGAGTTCAAGACCAAGCTGGCCAAACATGTAAGAAACCCATCTCTA 134859
QY 2163 CTAAGAT 2170
DB 134860 CTAAGAT 134867

RESULT 58
LOCUS C0695774 330 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 40700 from Patent WO02070737.
ACCESSION C0695774
VERSION C0695774.1 GI:42243043

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS Llew.C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 40700 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
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/organism="Homo sapiens"
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QY 2105 TCATCTGAGGTCAGAGTTCAGAGCCAGCTGCGCAACATGCTGAACCCCATCTCTACT 2164
Db 113 TCATCTGAGGTCAGAGTTCAGAGCCAGCTGCGCAACATGCTGAACCCCATCTCTACT 172
QY 2165 AAA 2167
Db 173 AAA 175
RESULT 59
LOCUS CO414086 976 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 21157 from Patent WO0170979.
ACCESSION CO414086
VERSION CO414086.1 GI:41321867
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS Lee,J. and Little,J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 21157 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2165 AAA 2167
Db 827 AAA 829
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LOCUS HSA131341 9507 bp DNA linear PRI 01-FEB-1999
DEFINITION Homo sapiens ogg1 gene, exons 1-7.
ACCESSION AJ131341
VERSION AJ131341.1 GI:4210713

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS Dhenaut,A., Boileux,S. and Radicella,J.
TITLE Genomic structure and promoter characterization of the human
JOURNAL 8-OH-guanine glycosylase gene (OGG1) gene
Unpublished
2 (bases 1 to 9507)
Radicella,J.
REFERENCE
1
AUTHORS Submitted (05-DEC-1998) Radicella J., Departement de Radiobiologie
et Radiopathologie, Commissariat a l' Energie Atomique, 60 Avenue
du general Leclerc, Fontenay aux Roses, F 92265, FRANCE
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/db_xref="GOA:O15527"
/db_xref="Swiss-Prot:O15527"
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LVTTLAQLVHMGVSVDHSEVAKQKPGCRLLRQPIELTFSFICSSNNINIRITGMV
EELCOAFGRRLQLQDDVYTRGPPSLQALAGPEVBAHRLKRGIRRYASARALE
EGGLAWLQQLKSSSTBEAHKALCTIPGVGTVAUDCTLWALDKPDQAVVDVHMHIA
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/number=3
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6868..8452
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8453..8603
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8604..8748

exon	/gene="Oggl" /number=5 8749. .8798 /gene="Oggl" /number=6 8799. .9042 /gene="Oggl" /number=6 9043. .9393 /gene="Oggl" /number=7
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exon	
ORIGIN	
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Best Local Similarity	100.0%; Prid. No. 6e-25;
Matches	63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	2105 TCATCTGAGTCAGAGATTCAAGACCAAGCCGGCCAAACATGATGTAACCCCATCTTACT 2164 Db 4812 TCATCTGAGTCAGAGATTCAAGACCAAGCCGGCCAAACATGATGTAACCCCATCTTACT 4871
OY	2165 AAA 2167 Db 4872 AAA 4874
RESULT 61	
AF521807	10461 bp DNA linear PRI 02-JUN-2002
LOCUS	
DEFINITION	Homo sapiens 8-oxoguanine DNA glycosylase (OGG1) gene, complete
ACCESSION	AF521807
VERSION	AF521807.1 GI:21668117
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 10461) Rider, M. J., Livingston, R. J., Braun, A. C., Montoya, M. A., Chung, M. W., Miyamoto, K. E., Nguyen, C. P., Nguyen, D. A., Poel, C. L., Robertson, P. D., Schackwitz, W. S., Sherwood, J. K., Witrak, L. A. and Nickerson, D. A. Direct Submission Submitted (14-JUN-2002) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA To cite this work please use: NIEHS-SNPs, Environmental Genome Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://esp.gs.washington.edu).
COMMENT	
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variation	
variation	
variation	
variation	
repeat_region	

variation	/rpt_family="Alu" 940 /frequency="0.03" /replace="c" 1116. .9498 /gene="OGG1" join(1116. .2517,3040. .3287,3865. .4044,6799. .6980, 8566. .8716,8862. .8911,9156. .9498) /gene="OGG1" product="8-oxoguanine DNA glycosylase" 1754 /gene="OGG1" /frequency="0.01" /replace="c" 2077. .2079 /gene="OGG1" /frequency="0.01" /replace="n" 2101 /gene="OGG1" /frequency="0.03" /replace="g" 2363 /gene="OGG1" /frequency="0.01" /replace="c" join(12381. .2517,3040. .3287,3865. .4044,6799. .6980, 8566. .8716,8862. .8911,9156. .9245) /gene="OGG1" /codon_start=1 /product="8-oxoguanine DNA glycosylase" /protein_id="AAW74236.1" /db_xref="GI:21668118" translation="MPARALLPRMGHRTLASTPALWASIPCPRESELRDLVLPSCGS FRMEGSAHSGVLADQWMLTQTEQLHCTVYRGKSGASRPTPELAVARKYFOL DVTIAQLYHNHGSDSHFQEVAKQFQGVRLLRDPIECLEFICSSNNINARIATGWE RLCQAFQGRLLQLDDVTYHGFPSLDALAGEVEAHLEKLGITRARIYVSASARILIEE RGLQAWLDQQLKESSYEBAHKALCILPGVGTKVAQCILMALDKQAIVPVHMHQIAE RDYWMHPTTSSQAKPSPQTNKELGNFFRSIMGPYAGWAQAVLFSADLRQSRHAQEPRA KRRGSKKPEG"
repeat_region	2736. .2921 /rpt_family="Alu" /rpt_type=dispersed 2812
variation	/gene="OGG1" /frequency="0.91" /replace="n" 2828
variation	/gene="OGG1" /frequency="0.01" /replace="c" 3320. .3478 /rpt_family="MIR" /rpt_type=dispersed 3413
repeat_region	/gene="OGG1" /frequency="0.01" /replace="g" 3551. .3651 /rpt_family="L2" /rpt_type=dispersed 4288. .4519 /rpt_family="MIR" /rpt_type=dispersed 4591. .4647 /rpt_family="Alu" /rpt_type=dispersed 4611
variation	/gene="OGG1" /frequency="0.01" /replace="c" 4751


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/gene="OGG1"
/refrequency="0.01"
/replacement="g"
repeat_region
4864..5160
/rpt_family="Alu"
/rpt_type=dispersed
variation
4931
/gene="OGG1"
/refrequency="0.01"
/replacement="g"
/misc_feature
5082..5789
/gene="OGG1"
/region not scanned for variation"
5165..5462
/rpt_family="Alu"
/rpt_type=dispersed
repeat_region
5466..5766
/rpt_family="Alu"
/rpt_type=dispersed
repeat_region
5770..5863
/rpt_family="MIR"
/rpt_type=dispersed
variation
5859
/gene="OGG1"
/refrequency="0.03"
/replacement="g"
repeat_region
5917..5949
/rpt_family="MIR"
/rpt_type=dispersed
variation
5924
/gene="OGG1"
/refrequency="0.01"
/replacement="a"
repeat_region
5950..6247
/rpt_family="Alu"
/rpt_type=dispersed
variation
5954
/gene="OGG1"
/refrequency="0.42"
/replacement="g"
repeat_region
6248..6470
/rpt_family="MIR"
/rpt_type=dispersed
variation
6350
/gene="OGG1"
/refrequency="0.01"
/replacement="g"
variation
6537
/gene="OGG1"
/refrequency="0.11"
/replacement="g"
variation
6919
/gene="OGG1"
/refrequency="0.03"
/replacement="a"
variation
7224
/gene="OGG1"
/refrequency="0.01"
/replacement="g"
repeat_region
7315..7457
/rpt_family="Alu"
/rpt_type=dispersed
repeat_region
7555..7854
/rpt_family="Alu"
/rpt_type=dispersed
repeat_region
7919..8066
/rpt_family="MIR"
/rpt_type=dispersed
misc_feature
7951..8151
/gene="OGG1"
/region not scanned for variation"
8130..8415
/rpt_family="Alu"

```

```

variation
8253
/gene="OGG1"
/refrequency="0.01"
/replacement="g"
variation
8551
/gene="OGG1"
/refrequency="0.35"
/replacement="g"

Query Match      2.3% Score 63; DB 9; Length 10461;
Best local Similarity 100.0%; Pred. No. 66-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2105 TCATCTGAGGTGAGGCTTCAAGACGAGCTGGCCAACTGGGAAACCCCATCTACT 2164
         |||||
Db      4924 TCATCTGAGGTGAGGCTTCAAGACGAGCTGGCCAACTGGGAAACCCCATCTACT 4983

Qy      2165 AAA 2167
         |||
Db      4984 AAA 4986

RESULT 62
AC004224/c      41495 bp DNA linear PRI 26-FEB-1998
LOCUS           Homo sapiens chromosome 16, cosmid clone 30655 (LNU), complete
DEFINITION
ACCESSION      AC004224
VERSION        AC004224.1 GI:2911722
KEYWORDS       HTG.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS        1 (bases 1 to 41495)
               Ricke,D.O., Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E.,
               Robinson,D., Jones,M., Buckingham,J., Chasteen,L., Thompson,S.,
               Goodwin,L., Bryant,J., Tesmer,J., Meincke,L., Longfibre,J.,
               White,S., Deng,S., Tatum,O., Campbell,C., Fawcett,J., McBride,M.,
               Mista,M. and Deaven,L.
               Sequencing of Human Chromosome 16p13.3
TITLE           Comparison Analysis (SCAN) System
JOURNAL         Unpublished
REFERENCE
AUTHORS        2 (bases 1 to 41495)
               Ricke,D.O., Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E.,
               Robinson,D., Jones,M., Buckingham,J., Chasteen,L., Thompson,S.,
               Goodwin,L., Bryant,J., Tesmer,J., Meincke,L., Longfibre,J.,
               White,S., Deng,S., Tatum,O., Campbell,C., Fawcett,J., McBride,M.,
               Mista,M. and Deaven,L.
TITLE           Direct Submission
JOURNAL         Submitted (26-FEB-1998) Center for Human Genome Studies, DOE Joint
               Genome Institute, Los Alamos National Laboratory, MS M888, Los
               Alamos, NM 87545, USA
FEATURES
source         1..41495
               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
               /clone="30655"
               /complement(263..580)
               /rpt_family="Alu"
               /complement(637..770)
               /note="GRAIL 2 excellent exon, frame 0"
               /complement(2535..3063)
               /rpt_family="MER42c"
               /complement(3062..3558)
               /rpt_family="Alu"
               /complement(3615..4184)

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repeat_region /rpt_family="MERA2"
complement(4529..4603)
misc_feature /rpt_family="MIR"
complement(5082..5165)
repeat_region /note="GRAIL 2 excellent exon, frame 0"
complement(5463..5601)
repeat_region /rpt_family="Alu"
5834..6126
/rpt_family="MLT1a"
6924..7238
repeat_region /rpt_family="Alu"
7685..8044
/rpt_family="Alu"
complement(8195..8290)
misc_feature /note="GRAIL 2 excellent exon, frame 1"
complement(8333..8768)
repeat_region /rpt_family="Alu"
complement(9058..9423)
misc_feature /note="97% identity Hc817-F"
/db_xref="dbEST:R15682"
repeat_region /rpt_family="MERA3"
complement(9909..10066)
10235..10853
/rpt_family="Alu"
complement(11409..11709)
repeat_region /rpt_family="Alu"
complement(11756..11848)
misc_feature /note="GRAIL 2 good exon, frame 1"
complement(12185..12384)
misc_feature /note="GRAIL 2 excellent exon, frame 2"
complement(12209..12385)
/note="100% identity BST56793"
/db_xref="dbEST:AA349832"
12955..12992
/note="CA19"
repeat_region /rpt_type=tandem
/rpt_unit="T"
complement(13084..13382)
repeat_region /rpt_family="Alu"
complement(13440..13762)
repeat_region /rpt_family="Alu"
13852..14173
/rpt_family="Alu"
complement(14258..14342)
misc_feature /note="GRAIL 2 excellent exon, frame 1"
complement(15093..15693)
repeat_region /rpt_family="Alu"
15103..15126
/note="(T)24"
repeat_region /rpt_type=tandem
/rpt_unit="T"
complement(15814..15953)
misc_feature /note="GRAIL 2 excellent exon, frame 2"
16899..17200
/rpt_family="Alu"
repeat_region /rpt_family="Alu"
17211..17692
/rpt_family="Alu"
complement(18196..18512)
repeat_region /rpt_family="Alu"
18626..18824
/rpt_family="MTR"
complement(18874..19172)
repeat_region /rpt_family="Alu"
complement(19284..19383)
repeat_region /rpt_family="MERA3"
20003..20306
/rpt_family="AluSg"
20285..20306
/note="(A)22"
repeat_region /rpt_type=tandem
/rpt_unit="A"
complement(21312..21518)
repeat_region /rpt_family="AluSg"

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repeat_region 21539..21654
/rpt_family="RBL10C4"
complement(21787..22166)
repeat_region /rpt_family="Alu"
21787..21809
/note="(GTT)6"
repeat_region /rpt_type=tandem
/rpt_unit="GTT"
22250..22717
/rpt_family="MLT2B2"
22717..23047
repeat_region /rpt_family="AluBc"
23504..23811
/rpt_family="AluSx"
complement(23866..24389)
misc_feature /note="88% identity ribosomal protein L18"
24248..24399
/note="GRAIL 2 excellent exon, frame 1"
complement(24498..24849)
repeat_region /rpt_family="Alu"
25796..25984
/note="GRAIL 2 excellent exon, frame 0"
25893..25952
/note="90% identity mouse mc50c05.r1"
/db_xref="dbEST:W40826"
26396..26470
/rpt_family="MIR"
complement(27444..27976)
repeat_region /rpt_family="Alu"
27597..27616
/note="(T)20"
repeat_region /rpt_type=tandem
/rpt_unit="T"
complement(28269..28417)
/rpt_family="MERA20"
28455..28610
/rpt_family="MSTA"
28628..28923
/rpt_family="Alu"
complement(28970..29118)
repeat_region /rpt_family="Alu"
29046..29140
/rpt_family="THE1"
complement(29825..30111)
repeat_region /rpt_family="Alu"
complement(30137..30690)
/rpt_family="Alu"
30241..30275
/note="(T)35"
repeat_region /rpt_type=tandem
/rpt_unit="T"
31246..31568
/rpt_family="Alu"
31528..31560
/note="(A)33"
repeat_region /rpt_type=tandem
/rpt_unit="A"
31816..32140
/rpt_family="Alu"
complement(33287..33557)
repeat_region /rpt_family="Alu"
33720..34053
/standard name="W1-13763"
/db_xref="dbSTS:G82780"
33722..34151
/note="99% identity z652b07.s1"
/db_xref="dbEST:AA017253"
complement(join(35811..35973,38079..38173,41074..41219))
/standard name="fmc43"
/note="97% identity AA631976"
complement(35822..35911)
/note="GRAIL 2 excellent exon, frame 2"
36783..36910
repeat_region

```

```
/rpt_family="Alu"
prim_transcript complement(join(37073..37312,38073..38170))
/standard_name="ms33a04"
/notes="89% identity AL169004 mouse EST ms33a04.r1"
misc_feature
/notes="GRAIL 2 excellent exon, frame 2"

Query Match 2.3%; Score 63; DB 9; Length 41495;
Best Local Similarity 100.0%; Pred. No. 6.1e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2105 TCATCTGAGGTCAAGAGTTCAAGACAGCCTGCGCAATGATGTAACCCATCTTACT 2164
|||||
Db 40311 TCATCTGAGGTCAAGAGTTCAAGACAGCCTGCGCAATGATGTAACCCATCTTACT 40252

QY 2165 AAA 2167
|||
Db 40251 AAA 40249

RESULT 63
AL138915/c 42569 bp DNA linear PRI 01-NOV-2000
LOCUS Human DNA sequence from clone RP11-288K24 on chromosome 6, complete
DEFINITION
ACCESSION AL138915
VERSION AL138915
KEYWORDS GI:11120994
SOURCE HTG.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 42569)
Almeida,J.
Direct Submission
Submitted (31-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequests@sanger.ac.uk
On Nov 8, 2000 this sequence version replaced gi:10800462.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
Chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
RP11-288K24 is from the library RPCI-11.1 constructed at the
Roswell Park Cancer Institute by the group of Peter de Jong. For
further details see http://bacpac.med.buffalo.edu/
VECTOR: pBACE3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-288K24. It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true right end of clone RP11-288K24 is at 42569 in this
sequence. The true left end of clone RP11-44004 is at 4198 in this
sequence. The true right end of clone RP4-810P7 is at 100 in this
sequence.
```

```
FEATURES
Source 1..42569
Location/Qualifiers
```

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RP11-288K24"
/clone_lib="RPCI-11.1"
413..721
/notes="AluY repeat: matches 3..311 of consensus"
895..940
/notes="23 copies 2 mer aa 80% conserved"
1031..1106
/notes="L2 repeat: matches 2629..2703 of consensus"
complement(3732..4196)
/notes="match: GSS: Em:AQ826809"
4334..4548
/notes="MER30 repeat: matches 1..229 of consensus"
5443..5585
/notes="MIR repeat: matches 11..147 of consensus"
5696..5997
/notes="MER2 repeat: matches 1..344 of consensus"
complement(6322..6908)
/notes="match: GSS: Em:AQ108173"
6524..6647
/notes="62 copies 2 mer aa 58% conserved"
6708..6860
/notes="L2 repeat: matches 2248..2402 of consensus"
7232..7412
/notes="MER5B repeat: matches 1..172 of consensus"
7703..7871
/notes="MIR repeat: matches 1..187 of consensus"
9463..9611
/notes="L2 repeat: matches 2553..2710 of consensus"
9729..10019
/notes="AluSG repeat: matches 1..289 of consensus"
10186..10401
/notes="L2 repeat: matches 1992..2238 of consensus"
10612..11234
/notes="match: GSS: Em:AQ485652"
10897..10971
/notes="L2 repeat: matches 2623..2698 of consensus"
10981..11160
/notes="AluSG/X repeat: matches 117..292 of consensus"
complement(11156..11348)
/notes="match: GSS: Em:A2335903"
11161..11244
/notes="42 copies 2 mer ta 81% conserved"
11256..11303
/notes="24 copies 2 mer ta 77% conserved"
11711..12009
/notes="AluSX repeat: matches 4..302 of consensus"
12010..13625
/notes="L1PA2 repeat: matches 4528..6144 of consensus"
13628..13695
/notes="34 copies 2 mer aa 69% conserved"
complement(13655..13792)
/notes="Sequence derived only from overlapping clone
Alu39093. Assembly confirmed by restriction digest."
14176..14515
/notes="MER6A repeat: matches 2..331 of consensus"
14516..14822
/notes="AluSX repeat: matches 3..311 of consensus"
14823..15068
/notes="MER6A repeat: matches 331..605 of consensus"
15161..15766
/notes="match: GSS: Em:AQ634114"
15178..15677
/notes="match: GSS: Em:AQ634115"
16512..16969
/notes="match: GSS: Em:AQ775062"
complement(16633..17263)
/notes="match: GSS: Em:AQ029865"
complement(16778..17263)
/notes="match: GSS: Em:AQ309773"
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repeat_region	18485..18681	/note="L2 repeat: matches 2547..2749 of consensus"
repeat_region	18782..19127	/note="L2 repeat: matches 1992..2401 of consensus"
repeat_region	19343..19596	/note="L2 repeat: matches 5621..5892 of consensus"
repeat_region	19870..20190	/note="L2 repeat: matches 1480..1835 of consensus"
repeat_region	21836..21970	/note="L2 repeat: matches 1135..1270 of consensus"
misc_feature	23109	/note="match: GSS: Em:AQ007507"
misc_feature	23154..24018	/note="match: GSS: Em:AQ739487"
misc_feature	23178..24018	/note="match: GSS: Em:AQ739128"
repeat_region	26154..26235	/note="L2 repeat: matches 2642..2709 of consensus"
misc_feature	26491..27075	/note="match: GSS: Em:AQ351931"
repeat_region	26735..26822	/note="L2 repeat: matches 4 mer atag 84% conserved"
repeat_region	26855..27598	/note="L2 repeat: matches 5376..6159 of consensus"
repeat_region	27599..27905	/note="L2 repeat: matches 3..308 of consensus"
repeat_region	27906..27927	/note="L2 repeat: matches 5356..5376 of consensus"
repeat_region	27985..28284	/note="L2 repeat: matches 1..300 of consensus"
repeat_region	28305..28901	/note="L2 repeat: matches 3628..5333 of consensus"
repeat_region	29927..30317	/note="L2 repeat: matches 2887..3304 of consensus"
misc_feature	30512	/note="match: GSS: Em:AQ390818"
misc_feature	30517..30512	/note="match: GSS: Em:AQ390890"
repeat_region	31076..31512	/note="L2 repeat: matches 57..543 of consensus"
repeat_region	31609..31644	/note="L2 repeat: matches 83% conserved"
repeat_region	31645..31704	/note="L2 repeat: matches 4 mer gata 70% conserved"
repeat_region	31774..32115	/note="L2 repeat: matches 1514..1853 of consensus"
repeat_region	32128..32183	/note="L2 repeat: matches 73% conserved"
repeat_region	32190..32183	/note="L2 repeat: matches 61..256 of consensus"
repeat_region	32221..32712	/note="L2 repeat: matches 2572..2744 of consensus"
repeat_region	32698..33046	/note="L2 repeat: matches 2560..2710 of consensus"
repeat_region	33361..33565	/note="L2 repeat: matches 9..106 of consensus"
repeat_region	33568..33627	/note="L2 repeat: matches 2579..2748 of consensus"
repeat_region	33824..33945	/note="L2 repeat: matches 2691..2749 of consensus"
repeat_region	34491..34588	/note="L2 repeat: matches 2560..2710 of consensus"
repeat_region	34928..35088	/note="L2 repeat: matches 2572..2744 of consensus"
misc_feature	35661..35669	/note="match: GSS: Em:AQ217519"
repeat_region	37561..37630	/note="L2 repeat: matches 2679..2748 of consensus"
repeat_region	37976..38226	/note="L2 repeat: matches 2..243 of consensus"
repeat_region	38728..39043	/note="L2 repeat: matches 2..243 of consensus"

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repeat_region /note="Aluub repeat: matches 5. .292 of consensus"
39906. .40158 /note="MLTII repeat: matches 238. .512 of consensus"

Query Match 2.3%: Score 63; DB 9; Length 42569;
Best Local Similarity 100.0%; Pred. No. 6,1e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2105 TCATCTGAGGTGACGAGTTCAGACCGCTGGCCAACATGTGGAAACCCCATCTTACT 2164
|||||
DB 28224 TCATCTGAGGTGACGAGTTCAGACCGCTGGCCAACATGTGGAAACCCCATCTTACT 28165

QY 2165 AAA 2167
|||
DB 28164 AAA 28162

RESULT 64
AC073932/c
LOCUS AC073932 48217 bp DNA linear PRI 10-JAN-2002
DEFINITION Homo sapiens BAC clone RP11-24207 from 4, complete sequence.
AC073932
VERSION AC073932.4 GI:18042387
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 48217)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
MEDLINE 9847074
PUBMED
REFERENCE 2 (bases 1 to 48217)
Trani,L., Cotton,M. and Creason,K.
The sequence of Homo sapiens BAC clone RP11-24207
Unpublished (2002)
JOURNAL 3 (bases 1 to 48217)
REFERENCE 3 (bases 1 to 48217)
Waterston,R.H.
Direct Submission
JOURNAL Submitted (03-JUN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 48217)
REFERENCE 4 (bases 1 to 48217)
Waterston,R.H.
Direct Submission
JOURNAL Submitted (03-JUN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 48217)
REFERENCE 5 (bases 1 to 48217)
Waterston,R.
Direct Submission
JOURNAL Submitted (10-JUN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 3, 2002 this sequence version replaced gi:17976485.
COMMENT -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics -----
Center project name: H_NH024207
-----

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., paired quality >=

```

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P. Y., Zhao, B., Frengen, E., Tatenno, M., Catanesse, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-36111, 2000 bp overlap; the clone sequenced to the right is RP11-36716, 2000 bp overlap.

Data from AC084049 was used to finish this clone AC073932. Polymorphisms exist between AC079257 and AC073932.

FEATURES**Source**

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5111..5130
/rpt_family="(TTTGG)n"
5544..5932
/rpt_family="MER1_type"
6062..6083
/rpt_family="(T)n"
6540..6869
/rpt_family="Alu"
6843..6884
/rpt_family="(TAA)n"
6926..6949
/rpt_family="(T)n"
6947..7258
/note="match to EST AW515568 (NID:G7153650) XU73C09.X1"
7018..7051
/rpt_family="T-rich"
7891..8258
/rpt_family="L1"
8279..8325

/rpt_family="MER1_type"
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9636..9782
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9783..10076
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10077..10240
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10533..10588
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10918..11458
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11612..11703
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11743..12665
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12019..12047
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12743..12953
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13267..13469
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14665..14975
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14976..15273
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15755..16046
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16368..16592
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Query Match 2.3%; Score 63; DB 9; Length 48217;
Best Local Similarity 100.0%; Pred. No. 6,2e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2105 TCATCTGAGGTGAGAGTTCAAGACCAAGCTGCGCAACATGCTGAACCCCATCTCTACT 2164
|||||
DB 15214 TCATCTGAGGTGAGAGTTCAAGACCAAGCTGCGCAACATGCTGAACCCCATCTCTACT 15155
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QY 2165 AAA 2167
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DB 15154 AAA 15152

RESULT 65
AF176815 51803 bp DNA linear PRI 23-DEC-1999
LOCUS Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene,
DEFINITION complete cds.
ACCESSION AF176815
VERSION AF176815.1 GI:6630864
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 51803)
Hu,S.N., Dong,W., Zeng,Y.X., Yu,J. and Yang,H.M.
TITLE Sequencing and Analyzing of BAC DNA on 3p26
JOURNAL Unpublished
2 (bases 1 to 51803)
Hu,S.N., Dong,W., Zeng,Y.X., Yu,J. and Yang,H.M.
AUTHORS Direct Submission
TITLE Submitted (10-AUG-1999) Human Genomic Center, Institute of
JOURNAL Genetics, Chinese Academy of Sciences, Datun Road, Beijing 100101,
P.R.China

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source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p26"
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34167..34295,35086..35395,35720..36043,36366..36650,
37150..37297,37715..37851,37954..38072,38442..38596,
39308..39491)
/product="putative 8-hydroxyguanine DNA glycosylase"
join(26286..26884,31142..32101,32922..33084,33451..33582,
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/protein_id="AAPI9605.1"
/db_xref="GI:6630865"
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NHHHHNVASSTTPKLEVVYRELEQDTPDAPRPSTYRYLEKSEELDEVEVDM
EDBYIWLIDINNERKTEGVSPFOELFEVIMDLREKESYFESGNKDDPALVADAVC
CICNDECONSNVILFCDMCNLAHOECYGVYIPFGOMLCRCLCSPERAVCALCP
NGGAFKOTDDGMAHVCAIMPEVCFANTVFLBIDSIENHPPARKLTCYICKOR
GSGACTOCHKANCYTAFTYTCQAQAGLYAKMEPVRTGANGSFSRKTAYYDITRP
GSAKRLPALSHSDEDEDEDEDEBEGKMSSEKVKAKAKSRIKMKAKYLIEKRAAA
PVVSPCIPPHRLSKITNRLTIQRKSQFMORLSYWTLRQSRNGVPLRLRQTHLS
ORNCQVGRDSEDKMNLKEOLSKMQLRHDLERALLVELIRKREKLRKETIKYQOI
AMEMOITPLILRLTLEOLEKDTGNIPSEPPLESDYDLNHIKKPMDPTMKONT
BAVRYLNDPDEEDENLIVSNCLKYNAKTTITYRAVRLRBOGANTLROARQAEKMG
IDPETGMHITPHSLAGDEATHHTEDAAEEERLVLLEOKHLPVBEOLKLLBRUDEYNA
SKOSVGRSRRAKMTKKEMLARKKLAKHQETGDEPERGSPSSRSLTHTHPACDDG
QDSDAAESSQETSIGLGPNNMSTPAHVEGRTSYLFSKKNPKTAGPPKRPGRPPKN

RESQWTPSHGSGPVGPPQLPIMSLSLRQKRRGRSPRSSSSSDSDSKTEDEPMDIPAN
GFGSGNQVKKKSFLVYRNDCLSPRSSDSESSSSSSSSAAADRTSTTSKQGRKPSF
SRGTPEPDSSTGCTENEAAYSVGSGSRMYSKSLRGAGMILSEDEDSPLDALDL
VMKRCRGYSYPALIIDPKMREGFHGVIPVPPLEVLKGEOMTEAREHVLVL
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FOSSETSDSD"

Query Match 2.3%; Score 63; DB 9; Length 51803;
Best Local Similarity 100.0%; Pred. No. 6,2e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2105 TCATCTGAGGTGAGAGTTCAAGACCAAGCTGCGCAACATGCTGAACCCCATCTCTACT 2164
|||||
DB 44971 TCATCTGAGGTGAGAGTTCAAGACCAAGCTGCGCAACATGCTGAACCCCATCTCTACT 45030
|||||

QY 2165 AAA 2167
|||
DB 45031 AAA 45033

RESULT 66
AC002506/c 54659 bp DNA linear HTG 13-JUN-2002
LOCUS Homo sapiens clone 440B5, *** SEQUENCING IN PROGRESS ***
DEFINITION unorderd pieces.
ACCESSION AC002506
VERSION AC002506.2 GI:21408066
KEYWORDS HTG; HTGS_PHASE1
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 54659)
Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R.,
Fuhmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L.,
Deslattes Mays,A., Cao,Y., Xu,R.X., Kang,H.L., Mitchell,S.,
Eichler,E.E., Harris,P.C., Venter,J.C. and Adams,M.D.
TITLE Genome duplications and other features in 12 Mb of DNA sequence
JOURNAL from human chromosome 16p and 16q
MEDLINE Genomics 60 (3), 295-308 (1999)
PUBMED 99425270
10493829
2 (bases 1 to 54659)
Adams,M.D., Loftus,B.J., Zhou,L., Phillips,C., Brandon,R.C.,
Fuhmann,J., Kim,U.J., Kerlavage,A.R. and Venter,J.C.
AUTHORS Human chromosome 16p13 BAC clone LANL cosmid-440B5
TITLE Unpublished
3 (bases 1 to 54659)
Adams,M.D.
REFERENCE Direct Submission
TITLE Submitted (26-AUG-1997) The Institute for Genomic Research, 9712
JOURNAL Medical Center Dr, Rockville, MD 20850, USA
On Jun 13, 2002 this sequence version replaced gi:2623293.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 2418: contig of 2418 bp in length
* 2419 19809: gap of unknown length
19810 54659: contig of 34850 bp in length.
Location/Qualifiers
1..54659
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/db_xref="taxon:9606"
/clone="440B5"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 6.2e-25;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2105 TCATCTGAGGTGAGGAGTTCAAGACCAAGCCCTGGCCAAATGTTGAAAACCCCATCTTACT 2164
 46338 TCATCTGAGGTGAGGAGTTCAAGACCAAGCCCTGGCCAAATGTTGAAAACCCCATCTTACT 46279

Qy 2165 AAA 2167
 46278 AAA 46276

Db 46278 AAA 46276

RESULT 67
 HS342B11 56458 bp DNA linear PRI 04-MAR-2003
 LOCUS Human DNA sequence from clone CTA-342B11 on chromosome
 DEFINITION 22q12.1-12.3, complete sequence.
 ACCESSION AL008719
 VERSION AL008719.1 GI:3550041
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 56458)
 Clark, G.
 Direct Submission
 Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk
 On Sep 8, 1998 this sequence version replaced gi:3242181.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em, EMBL; SW, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
 on the WORMPEP database can be found at
 http://www.sanger.ac.uk/projects/C_elegans/wormpep
 CTA-342B11 is
 from the human BAC library described in U-U. Kim et al. (1996)
 Genomics 34, 213-218.
 VECTOR: pBAC108L

----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquerry@sanger.ac.uk

 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest, except on the rare
 occasion of the clone being a YAC.
 This sequence was generated from part of bacterial clone contigs of
 human chromosome 22, constructed by the Sanger Centre Chromosome 22
 Mapping Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr22.
 Location/Qualifiers

FEATURES
 Source 1..56458
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="22"
 /map="q12.1-12.3"
 /clone="CTA-342B11"
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ORIGIN

Query Match 2.3%; Score 63; DB 9; Length 56458;
 Best Local Similarity 100.0%; Pred. No. 6.2e-25;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2105 TCATCTGAGGTGAGGAGTTCAAGACCAAGCCCTGGCCAAATGTTGAAAACCCCATCTTACT 2164
 25894 TCATCTGAGGTGAGGAGTTCAAGACCAAGCCCTGGCCAAATGTTGAAAACCCCATCTTACT 25953

Qy 2165 AAA 2167
 25954 AAA 25956

Db 25954 AAA 25956

RESULT 68
 AC044883/c 57851 bp DNA linear HTG 28-AUG-2002
 LOCUS Homo sapiens chromosome 12 clone RP11-714A22 map 12, LOW-PASS
 DEFINITION SEQUENCE SAMPLING.
 ACCESSION AC044883
 VERSION AC044883.1 GI:7543850
 KEYWORDS HTG; HTGS PHASE0.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 57851)
 Birren, B., Linton, L., Nuebaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Baettien, V., Beda, F.,
 Bogunlavsky, L., Boukhalter, B., Brown, A., Burkett, G.,
 Campiano, A., Casale, A., Choepel, Y., Colangelo, M., Collins, S.,
 Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,
 Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
 Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
 Grand-Pierre, N., Grant, G., Hagos, B., Heatford, A., Horton, L.,
 Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
 Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehocsky, J.,
 Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Marguies, R.,
 McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPherson, R.,
 McElrath, J., Menus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J.,
 Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
 Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
 Testaye, S., Theodore, J., Tittell, A., Travers, M., Triggillo, J.,
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.
 Direct Submission

TITLE Submitted (12-APR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 57851)

JOURNAL
 AUTHORS

REFERENCE
 AUTHORS

 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest, except on the rare
 occasion of the clone being a YAC.
 This sequence was generated from part of bacterial clone contigs of
 human chromosome 22, constructed by the Sanger Centre Chromosome 22
 Mapping Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr22.
 Location/Qualifiers

FEATURES
 Source 1..56458
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="22"
 /map="q12.1-12.3"
 /clone="CTA-342B11"
 /clone_lib="CIT978SK-A1"

TITLE
JOURNAL
COMMENT

Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigglio, J.,
Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (28-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu

Project Information
Center project name: L9583
Center Clone name: 714_A_22

NOTE: This record contains 70 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 721: contig of 721 bp in length
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* 3228 3327: gap of 100 bp
* 3328 4057: contig of 730 bp in length
* 4058 4157: gap of 100 bp
* 4158 4868: contig of 711 bp in length
* 4869 4968: gap of 100 bp
* 4969 5687: contig of 719 bp in length
* 5688 5787: gap of 100 bp
* 5788 6477: contig of 690 bp in length
* 6478 6577: gap of 100 bp
* 6578 7287: contig of 710 bp in length
* 7288 7387: gap of 100 bp
* 7388 8147: contig of 760 bp in length
* 8148 8247: gap of 100 bp
* 8248 9036: contig of 789 bp in length
* 9037 9136: gap of 100 bp
* 9137 9941: contig of 805 bp in length
* 9942 10041: gap of 100 bp
* 10042 10724: contig of 683 bp in length
* 10725 10824: gap of 100 bp
* 10825 11549: contig of 725 bp in length
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* 17236 17335: gap of 100 bp

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* 19776 19875: gap of 100 bp
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* 20587 20686: gap of 100 bp
* 20687 21431: contig of 745 bp in length
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* 22346 23055: contig of 710 bp in length
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* 32411 32510: gap of 100 bp
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* 33283 33959: contig of 677 bp in length
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* 34899 35656: contig of 758 bp in length
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* 35757 36448: contig of 692 bp in length
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* 36549 37313: contig of 765 bp in length
* 37314 37413: gap of 100 bp
* 37414 38197: contig of 784 bp in length
* 38198 38297: gap of 100 bp
* 38298 39019: contig of 722 bp in length
* 39020 39119: gap of 100 bp
* 39120 39836: contig of 717 bp in length
* 39837 39936: gap of 100 bp
* 39937 40639: contig of 703 bp in length
* 40640 40739: gap of 100 bp
* 40740 41377: contig of 638 bp in length
* 41378 41477: gap of 100 bp
* 41478 42165: contig of 688 bp in length
* 42166 42265: gap of 100 bp
* 42266 42970: contig of 705 bp in length
* 42971 43070: gap of 100 bp
* 43072 43844: contig of 774 bp in length
* 43845 43944: gap of 100 bp
* 43945 44663: contig of 719 bp in length
* 44664 44763: gap of 100 bp
* 44764 45453: contig of 690 bp in length
* 45454 46359: contig of 806 bp in length
* 46360 46459: gap of 100 bp
* 46460 47193: contig of 734 bp in length

Query Match

2.3%; Score 63; DB 2; Length 57851;

Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2105 TCATCTGAGGTCAAGAGTTCAAGACCGCCTGGCCCAACATGTGTAACCCCATCTTACT 2164
DB 8430 TCATCTGAGGTCAAGAGTTCAAGACCGCCTGGCCCAACATGTGTAACCCCATCTTACT 8371

QY 2165 AAA 2167
DB 8370 AAA 8368

RESULT 69
BX511044.6
WPCOMMENT

Sequence split into 7 fragments LOCUS BX511044 Accession BX511044
Fragment Name Begin End
BX511044_0 1 110000
BX511044_1 100001 210000
BX511044_2 200001 310000
BX511044_3 300001 410000
BX511044_4 400001 510000
BX511044_5 500001 610000
BX511044_6 600001 663813
Continuation (7 of 7) of BX511044 from base 600001 (BX511044 Homo sapiens chromosome 1 c

Query Match 2.3%; Score 63; DB 2; Length 63813;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2105 TCATCTGAGGTCAAGAGTTCAAGACCGCCTGGCCCAACATGTGTAACCCCATCTTACT 2164
DB 4249 TCATCTGAGGTCAAGAGTTCAAGACCGCCTGGCCCAACATGTGTAACCCCATCTTACT 4308

QY 2165 AAA 2167
DB 4309 AAA 4311

RESULT 70
HSJ168B21/c

LOCUS HSJ168B21 67973 bp DNA linear PRI 04-MAR-2003
DEFINITION Human DNA sequence from clone RP1-168B21 on chromosome 6q26-27,
complete sequence.

ACCESSION AL118518 GI:6911654
VERSION AL118518.13
KEYWORDS HTG.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 67973)

REFERENCE Tracey, A.
AUTHORS Direct Submission
TITLE Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
JOURNAL humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT On Feb 7, 2000 this sequence version replaced g1:6822187.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
RP1-168B21 is from the library RP1-1 constructed by the group of
Pleter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.

FEATURES

source
1..67973
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="q26-27"
/clone="RP1-168B21"
/clone_11b="RP1-1"

ORIGIN

Query Match 2.3%; Score 63; DB 9; Length 67973;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2105 TCATCTGAGGTCAAGAGTTCAAGACCGCCTGGCCCAACATGTGTAACCCCATCTTACT 2164
DB 54564 TCATCTGAGGTCAAGAGTTCAAGACCGCCTGGCCCAACATGTGTAACCCCATCTTACT 54505

QY 2165 AAA 2167
DB 54504 AAA 54502

RESULT 71
AC011113/c

LOCUS AC011113 68118 bp DNA linear HTG 28-NOV-2001
DEFINITION Homo sapiens clone RP11-11405, LOW-PASS SEQUENCE SAMPLING.

ACCESSION AC011113
VERSION AC011113.3 GI:17048143
KEYWORDS HTG; HTGS PHASE0.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 68118)

REFERENCE Birren, B., Linton, L., Nusbaum, C. and Lander, E.
AUTHORS 1 (bases 1 to 68118)
TITLE Homo sapiens, clone RP11-11405
JOURNAL Unpublished
2 (bases 1 to 68118)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barne, N., Beckerly, R., Boguslavsky, L., Bouhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., Deavellano, K., Dewar, K., Domingo, M., Donelan, L., Doyle, M.,
Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hages, B., Heath, A., Horton, L.,
Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Liu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Melidre, J.,
Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testaye, S., Tjirelli, A., Vasilev, H., Vo, A., Wheeler, J., Wu, X.,
Wymann, D., Ye, W., Zimmer, A. and Zody, M.
Direct Submission

TITLE

JOURNAL
Submitted (01-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 22, 2001 this sequence version replaced gi:581939.
COMMENT
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute / MIT Center for Genome Research
Genome Center

Center code: MIBR

Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L1960

Center clone name: 114_O_5

* NOTE: This record contains 84 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1
* 676 675: contig of 675 bp in length
* 776 775: gap of 100 bp
* 1500 1499: contig of 724 bp in length
* 1600 1599: gap of 100 bp
* 2320 2319: contig of 720 bp in length
* 2420 2419: gap of 100 bp
* 3142 3141: contig of 722 bp in length
* 3242 3241: gap of 100 bp
* 3948 3948: contig of 707 bp in length
* 4048 4048: gap of 100 bp
* 4049 4770: contig of 722 bp in length
* 4771 4870: gap of 100 bp
* 4871 5598: contig of 728 bp in length
* 5599 5698: gap of 100 bp
* 5699 6413: contig of 715 bp in length
* 6414 6513: gap of 100 bp
* 6514 7230: contig of 717 bp in length
* 7231 7330: gap of 100 bp
* 7331 8041: contig of 711 bp in length
* 8042 8141: gap of 100 bp
* 8142 8783: contig of 642 bp in length
* 8784 8883: gap of 100 bp
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* 9602 9701: gap of 100 bp
* 9702 10399: contig of 698 bp in length
* 10400 10499: gap of 100 bp
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* 11234 11333: gap of 100 bp
* 11334 12047: contig of 714 bp in length
* 12048 12147: gap of 100 bp
* 12148 12868: contig of 721 bp in length
* 12869 12968: gap of 100 bp
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* 13680 13779: gap of 100 bp
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* 14489 14588: gap of 100 bp
* 14589 15294: contig of 706 bp in length
* 15295 15394: gap of 100 bp
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* 16929 17028: gap of 100 bp
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* 17855 18516: contig of 662 bp in length
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* 22709 23411: contig of 703 bp in length
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* 25834 25933: gap of 100 bp
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* 26663 26762: gap of 100 bp
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* 29080 29179: gap of 100 bp
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* 30821 31533: contig of 713 bp in length
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* 36397 36496: gap of 100 bp
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* 37306 37999: contig of 694 bp in length
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* 41381 42090: contig of 710 bp in length
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* 44610 45322: contig of 713 bp in length
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* 47916 48642: contig of 727 bp in length
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*	48743	49451:	conf: of 719 bp	in length
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*	57559	57658:	gap of 100 bp	
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*	58379	58478:	gap of 100 bp	
*	58479	59135:	conf: of 717 bp	in length

Query Match	Score	DB 2;	Length
Best Local Similarity	100.0%	68118	68118

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2105	TCACTCTGAGTCAAGAGTTCAAGACCAAGCCTGGCCACATGGTGAAMCCCACTCTCTACT	2164
Db	51336	TCACTCTGAGTCAAGAGTTCAAGACCAAGCCTGGCCACATGGTGAAMCCCACTCTCTACT	51577

QY	2165	AAA	2167
Db	51576	AAA	51574

RESULT 72
AL359834

LOCUS	AL359834	70248 bp	DNA linear	PRI 03-DEC-2001
DEFINITION	Human DNA sequence from clone RP11-121P12 on chromosome 1, complete			

ACCESSION	AL359834
VERSION	AL359834.18
	GI:17384081

KEYWORDS	HTG.
SOURCE	Homo sapiens (human)
ORGANISM	

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo

REFERENCE 1 (bases 1 to 70248)

AUTHORS White, S.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-2001) Wellcome Trust Sanger Institute, Hinxton.

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Dec 5, 2001 this sequence version replaced g1:17154282.

During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL, Sw, ...

SWISSPROT: Tr, TREMBL; Mp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Ch1> Rpl1-12p12 is from the library RPl1-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACE3.6

IMPORTANT: This sequence is not the entire insert of clone RPl1-12p12. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RPl1-92G12 is at 68249 in this sequence. The true right end of clone RPl1-469A15 is at 2000 in this sequence.

Location/Qualifiers

SOURCE

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/organism="Homo sapiens"
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/chromosome="1"
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ORIGIN

Query Match Similarity 2.3%; Score 63; DB 9; Length 70248;
Best Local Similarity 100.0%; Pred. No. 6.2e+25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2105 TCATCTGAGGTGAGGATTCAGACCAGCCTGGCCAACTGTTGAACCCCATCTTCTACT 2164

QY |||||

21944 TCATCTGAGGTGAGGATTCAGACCAGCCTGGCCAACTGTTGAACCCCATCTTCTACT 25003

QY	2165	AAA	2167
Db	25004	AAA	25006

RESULT 73
AC139768/

LOCUS	AC139768	78491 bp	DNA	linear	PRI 26-MAR-2003
DEFINITION	Homo sapiens 12 BAC RP11-45485 (Roswell Park Cancer Institute Human)				

BAC Library) complete se
AC139768

VERSION AC139768.14 GI:29244593
KEYWORDS HTG.

SOURCE ORGANISM	Homo sapiens Homo sapiens <i>Eukaryota : Metazoa :</i>

1 (pages 1 to 78491)

AUTHORS

Barberia, J., Benson, J., Blmge, K., Blankenburg, K., Bonni, D.,
Bouch, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N. P.,
Buhay, C., Burch, P., Burnett, C., Burnett, K. L., Byrd, N. C.,
Carrion, T. F., Carter, M., Cavares, S. R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chin, D., Chowdhry, I., Christopoulos, C.,
Cleveland, C. D., Cox, C., Coyle, M. D., Dethorne, S. R., David, R.,
Davila, M. L., Davis, C., Davy-Carrroll, L., Dederich, D. A.,
Delaney, K. R., Delgado, O., Benn, A. L., Ding, Y., Dinh, H. H.,
Douthwaite, K. J., Draper, H., Dugan-Socha, S., Durbin, K. J.,
Earnhardt, C., Edgar, D., Edwards, C. C., Elhai, C., Emealing, S.,
Escotto, M., Fails, T., Ferrazuto, D., Flagg, N., Ford, J., Foster, P.,
Franz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N.,
Gill, R., Gorell, J. H., Guevara, W., Gunaratne, P., Hale, S.,
Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Haylak, P.,
Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M.,
Holloway, C., Hollins, B., Homeli, F., Howard, S., Huber, J., Hulak, S.,
Hume, J., Ishihara, I., Jackson, L. E., Jacobson, B., Jia, Y.,
Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U.,

King, L., Kovach, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Licharge, O., Lien, C., Liu, J., Liu, W., Louseged, H., Lozado, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapa, P., Maronde, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M. P., Meador, M., Mel, G., Merscher, S., Metzger, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K. T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokwkw, S., Oguni, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojudo, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shoohtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Uemami, K., Vaequez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Kuchelapati, R., Weinstock, G. and Gibbs, R.

TITLE Journal Submission

Unpublished

2 (bases 1 to 78491)

Worley, K.C.

Direct Submission

Submitted (13-FEB-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 78491)

Worley, K.C.

Direct Submission

Submitted (22-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

4 (bases 1 to 78491)

Worley, K.C.

Direct Submission

Submitted (26-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Mar 26, 2003 this sequence version replaced gi:29150318.

INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

COMMENT

AUTHORS

TITLE

JOURNAL

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Ref. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

FEATURES

source

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

misc_feature

/function="clone overlap" /note="overlaps bases 1..2004 of clone AC046135"

STS

/standard_name="D12S1951" /standard_name="A006B21"

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Best Local Similarity 100.0%; Pred. No. 6.2e-25; Mismatches 0; Indels 0; Gaps 0;

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65216 TCATCTGAGGTCAAGAGTTCAGACCAAGCTGGCCAACTGGTGAACCCCATCTCTACT 65157

QY 2165 AAA 2167
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Db 65156 AAA 65154

RESULT 74
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DEFINITION Sequence 1 from Patent WO03093826.
ACCESSION AX957048
VERSION AX957048.1 GI:40785349

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Benjamin, S., Clusel, C., Daur, A. and Escloux, L.
AUTHORS Assays for identifying cholesterol - lowering molecules
JOURNAL Patent: WO 03093826-A 1 13-NOV-2003;

FEATURES
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Location/Qualifiers

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QY 2165 AAA 2167
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Db 13306 AAA 13304

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LOCUS Homo sapiens genomic DNA, chromosome 11q clone: CMB9-40G4, complete
DEFINITION sequences.

ACCESSION AP000664
VERSION AP000664.4 GI:14189744
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Autori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Homo sapiens genomic DNA
Published Only in Database (1999)

REFERENCE 2 (bases 1 to 94779)
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission

JOURNAL Submitted (04-NOV-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suenho-chou, Tsukuba, Ibaraki, Japan
Tel: 81-45-503-9111, Fax: 81-45-503-9170
E-mail: hattori@gscc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
On May 22, 2001 this sequence version replaced gi:5798609.

FEATURES
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Location/Qualifiers

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/chromosome="11"
/map="11q"
/clone="CMB9-40G4"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 6.2e-25; Mismatches 0; Indels 0; Gaps 0;

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|||
Db 69172 TCATCTGAGGTCAAGAGTTCAGACCAAGCTGGCCAACTGGTGAACCCCATCTCTACT 69113
QY 2165 AAA 2167
|||
Db 69112 AAA 69110

Search completed: October 28, 2004, 17:01:05
Job time : 11370 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 13:07:25 ; Search time 8250 Seconds

(without alignments)
11943.338 Million cell updates/sec

Title: US-09-745-605-1

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

EST.*
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2: gb_sac2.*
3: gb_hnc.*
4: gb_sac3.*
5: gb_sac4.*
6: gb_sac5.*
7: gb_sac6.*
8: gb_gsa1.*
9: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	715	26.4	749	6	CD366342 UT-H-FT1-
C 3	697	25.8	767	6	CB529471 UT-H-FT2-
C 4	696	25.7	704	6	CB529490 UT-H-FT2-
C 5	674	24.9	731	6	CB986561 AGENCOURT
C 6	652	24.1	1035	4	BM549959 AGENCOURT
C 7	647	23.9	714	4	BG743853 AGENCOURT
C 8	646	23.9	738	6	CD364943 UT-H-FT2-
C 9	643	23.8	1043	5	BQ053807 AGENCOURT
C 10	632	23.4	904	5	BQ712547 AGENCOURT
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C 12	573	21.2	702	7	CN480770 UT-H-FT2-
C 13	572	21.2	648	6	CD687842 EST4363 h
C 14	567	21.0	602	1	A1638519 AGENCOURT
C 15	550	20.3	920	4	B1767020 AGENCOURT
C 16	545	20.2	760	6	CB956896 AGENCOURT
C 17	532	19.7	672	1	AM003948 AGENCOURT
C 18	527	19.5	739	6	CD366944 UT-H-FT2-
C 19	519	19.2	842	6	CD520950 AGENCOURT
C 20	515	19.0	1050	4	BM800975 AGENCOURT
C 21	512	18.9	785	6	CD366908 UT-H-FT2-
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C 39	373	13.8	614	1	AV733301
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/clone lib="NCI CGAP FT2"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN

25.8%; Score 697; DB 6; Length 767;

Query Match Best Local Similarity 100.0%; Pred. No. 1.1e-292; Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 585 GAGGATGTGATTATACCTGGAAGGCTGTGGGCAAGCAAGCAATGATGCTTCAATGGG 572
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FEATURES

source

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DEFINITION UI-H-FT2-bjh-a-16-0-UI 3', mRNA sequence.
ACCESSION CBS29490
VERSION CBS29490.1 GI:29390229
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 704)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=yes.

Location/Qualifiers
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TAG_TISSUE=Human Lung Alveolar Macrophage

QY 554 CAATGAGTCCCAATATGGTCCATCTCCCATCTCTGAGATGGGAGAAAGTATAT 613
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RESULT 6
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 VERSION BMS49959.1 GI:18785781
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1035)
 AUTHORS NIH-MGC http://img.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bms-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 High quality sequence stop: 663.
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 /note="Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
 (destroyed); RNA source leukocytes from anonymous pool of
 non-activated adult donors. Library is oligo-dT primed
 and directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 1.2-3.3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 027. Note:
 this is a NIH_MGC Library."

ORIGIN
 Query Match 24.1%; Score 652; DB 4; Length 1035;
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 Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 218 CCAAGAGGGGGGCACTATCTATGACCCCAAAATGTTATAGGAGAGTAGACTTCCA 277
 QY 294 GATGAGGCTACTCCCTGAGAGCTGACAACTGAAGAAATGACTCAGAGGATCTACTAT 353
 DB 278 GATGAGGCTACTCCCTGAGAGCTGACAACTGAAGAAATGACTCAGAGGATCTACTAT 337
 QY 354 GTGGGATATACAGCTCATCACTCCAGAGCCCTCCACCCAGAGTACGTGTCATGTC 413
 DB 338 GTGGGATATACAGCTCATCACTCCAGAGCCCTCCACCCAGAGTACGTGTCATGTC 397
 QY 414 TAGGACACCTGTCAAAGCTTAAGTCAACATGAGTCTGTCAGAGCATTAAGATGGCACC 473
 DB 398 TAGGACACCTGTCAAAGCTTAAGTCAACATGAGTCTGTCAGAGCATTAAGATGGCACC 457
 QY 474 TGTGACCAATCTGACATGCTGATGGAACATGGGAAAGAGATGATTTATACCTGG 533
 DB 458 TGTGACCAATCTGACATGCTGATGGAACATGGGAAAGAGATGATTTATACCTGG 517
 QY 534 AAGGCTCTGGGGCAAGCAGCCCAATGATGCCATTAATGGGTCATCTCCCATCTCTGG 593
 DB 518 AAGGCTCTGGGGCAAGCAGCCCAATGATGCCATTAATGGGTCATCTCCCATCTCTGG 577
 QY 594 AGATGGGGAAGAAAGTATATGACTTCTATCTGCGTTGGCCAGGAACCTGTGACGAGAAAC 653
 DB 578 AGATGGGGAAGAAAGTATATGACTTCTATCTGCGTTGGCCAGGAACCTGTGACGAGAAAC 637
 QY 654 TTCTCAAGGCCCATCTTCCAGGAAGCTCTGTGAAGGTGCTGATGACC 705
 DB 638 TTCTCAAGGCCCATCTTCCAGGAAGCTCTGTGAAGGTGCTGATGACC 689

RESULT 7
 BG743853
 LOCUS BG743853 714 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602722605F1 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:4849224 5',
 mRNA sequence.
 ACCESSION BG743853
 VERSION BG743853.1 GI:14054506
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 714)
 AUTHORS NIH-MGC http://img.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bms-r@mail.nih.gov
 Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM1688 row: i column: 01
 High quality sequence stop: 706.
 Location/Qualifiers
 1..714
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4849224"
 /issue_type="natural killer cells, cell line"
 /lab_host="DH10B (phage-resistant)"

FEATURES
 source

/clone_11b="NIH_MGC_106"
 /note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGAGG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

ORIGIN

Query Match 23.9%; Score 647; DB 4; Length 714;
 Best Local Similarity 100.0%; Pred. No. 7.4e-271;
 Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

44 GCGGTGTTCCCAACATGCTCCTCATTTATCTTTGGAGCTCACAGGCTACG 103
 2 GGGGTGTTCCCAACATGCTCCTCATTTATCTTTGGAGCTCACAGGCTACG 61
 104 AGCCTTGAGCCCGTGAAGAGCTGTGGTCCGTTGGTGGGCGGTGACCTTCCCT 163
 62 AGCCTTGAGCCCGTGAAGAGCTGTGGTCCGTTGGTGGGCGGTGACCTTCCCT 121
 164 GAACTCCAAAGTAAGCAAGTTGACTTATTTGTGACCTTCAACACACCCCTTGT 223
 122 GAAGTCCAAAGTAAGCAAGTTGACTTATTTGTGACCTTCAACACACCCCTTGT 181
 224 CACCATCAGCCAGAAAGGGGCACTATCATATGTAACCAAAATGTAATGGAGAGT 283
 182 CACCATCAGCCAGAAAGGGGCACTATCATATGTAACCAAAATGTAATGGAGAGT 241
 284 AGACTTCCAGATGAGAGGCTACTCCCTGAAGCTCAGAACTGAAGAAATGACTAG 343
 242 AGACTTCCAGATGAGAGGCTACTCCCTGAAGCTCAGAACTGAAGAAATGACTAG 301
 344 GATCTACTATGTGGGATATATACAGCTCATCACTCCAGAGCCCTCCACAGAGTAGT 403
 302 GATCTACTATGTGGGATATATACAGCTCATCACTCCAGAGCCCTCCACAGAGTAGT 361
 404 GCTGCATGTCTAGAGCACTGTGTCAAAAGCTCAACCAATGGGTTGCAAGCAATTA 463
 362 GCTGCATGTCTAGAGCACTGTGTCAAAAGCTCAACCAATGGGTTGCAAGCAATTA 421
 464 GAATGGCACTGTGTGCAATCTGATCTGTGATGGAACATGGGGAAGAGATGAT 523
 422 GAATGGCACTGTGTGCAATCTGATCTGTGATGGAACATGGGGAAGAGATGAT 481
 524 TTATACCTGGAAGCCCTGGGGCAAGCAGCAATGATCCCATTAATGGTCCATCTCC 583
 482 TTATACCTGGAAGCCCTGGGGCAAGCAGCAATGATCCCATTAATGGTCCATCTCC 541
 584 CATCTCTGAGATGGGGAAGAAAGTATATGATGATCTGCTGCTGCTCCAGAACTGT 643
 542 CATCTCTGAGATGGGGAAGAAAGTATATGATGATCTGCTGCTGCTCCAGAACTGT 601
 644 CAGCAGAAATCTTCAAGCCCATCTTGGCAGAGAACTCTTGAAG 690
 602 CAGCAGAAATCTTCAAGCCCATCTTGGCAGAGAACTCTTGAAG 648

RESULT 8
 CD364943/c 738 bp mRNA linear EST 05-AUG-2004
 LOCUS CD364943
 DEFINITION UI-H-FT2-bjn-k-01-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone
 UI-H-FT2-bjn-k-01-0-UI 3', mRNA sequence.
 ACCESSION CD364943
 VERSION CD364943.1 GI:31149033
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (Bases 1 to 738)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Straubeberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.iowa.edu/distribution/cgap.html>
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

Location/Qualifiers
 1..738
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FT2-bjn-k-01-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_11b="NCI CGAP FT2"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker. Site 1: EcoRI; Site 2: Not I; NCI CGAP FT2 is a subcloned cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subcloned according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
 TAG TISSUE=Human Lung Alveolar Macrophage
 TAG_LTB=UI-H-FT2
 TAG_SEQ=GGCATTGCCG"

ORIGIN

Query Match 23.9%; Score 646; DB 6; Length 738;
 Best Local Similarity 99.9%; Pred. No. 2e-270;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

393 CAGAGTAGCTGCTGATGTCACGACCTGTCAAGCTTAAGTCAACATGGGCTG 452
 705 CAGAGTAGCTGCTGATGTCACGACCTGTCAAGCTTAAGTCAACATGGGCTG 646
 453 CAGAGTAATGAATGAGCACTGTGACCAATCTGACATGCTGATGGAACATGGGGA 512
 645 CAGAGTAATGAATGAGCACTGTGACCAATCTGACATGCTGATGGAACATGGGGA 586
 513 GAGATGTGATTATATCTGGAAGGCCCTGGGGCAAGCAACCAATAGTCCCTAATGG 572
 585 GAGATGTGATTATATCTGGAAGGCCCTGGGGCAAGCAACCAATAGTCCCTAATGG 526
 573 TCCATCTCCCATCTCTGAGAGTGGGGAAGAAAGTATATGACCTTCACTGCGTTGC 632
 525 TCCATCTCCCATCTCTGAGAGTGGGGAAGAAAGTATATGACCTTCACTGCGTTGC 466

QY 633 AGGAACCCCTGTGACGAGAACTTCTACAGCCCCCATCTTGCAGAGAGCTGTGAAAGT 692
 Db 465 AGGAACCCCTGTGACGAGAACTTCTACAGCCCCCATCTTGCAGAGAGCTGTGAAAGT 406
 QY 693 GCTGCTGATGACCCAGATTCTTCATGATGATCTCTGTGTCTCTGTGTGCTCCCTCTG 752
 Db 405 GGTGCTGATGACCCAGATTCTTCATGATGATCTCTGTGTCTCTGTGTGCTCCCTCTG 346
 QY 753 CTCAGCTCTTGTGATGAGGAGCTATTTCTTGTGTTCTGTAAGAGAGAGACAAAGAG 812
 Db 345 CTCAGCTCTTGTGATGAGGAGCTATTTCTTGTGTTCTGTAAGAGAGAGACAAAGAG 286
 QY 813 TACATTGAAGAGAGAGAGAGTGAACATTTGTGCGGAAATCTCTTAACATATGCCCAT 872
 Db 285 TACATTGAAGAGAGAGAGAGTGAACATTTGTGCGGAAATCTCTTAACATATGCCCAT 226
 QY 873 TCTGAGAGAGACACAGAGTACAGACATCTCTCACATTAATGAACATCTCTAAAGAA 932
 Db 225 TCTGAGAGAGACACAGAGTACAGACATCTCTCACATTAATGAACATCTCTAAAGAA 166
 QY 933 GATCCAGAAATACGGTTTACTCTCACTGTGAAATACGAAAGATGAGAAATCCCCAC 992
 Db 165 GATCCAGAAATACGGTTTACTCTCACTGTGAAATACGAAAGATGAGAAATCCCCAC 106
 QY 993 TCACCTGCTCAGATGCGACAGACACCAAGCTATTGCTCTATGAGATGTATCTAGACA 1052
 Db 105 TCACCTGCTCAGATGCGACAGACACCAAGCTATTGCTCTATGAGATGTATCTAGACA 46
 QY 1053 GCAGTGCATCTCCCTTAAGTCTGTCTCAAAAAA 1089
 Db 45 GCAGTGCATCTCCCTTAAGTCTGTCTCAAAAAA 9

RESULT 9
 B0053807 1043 bp mRNA linear EST 29-MAR-2002
 LOCUS AGENCOURT_7027738 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5935701
 DEFINITION 5', mRNA sequence.
 ACCESSION B0053807
 VERSION B0053807.1 GI:19813147
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM2123 row: n column: 22
 High quality sequence stop: 610.
 Location/Qualifiers
 1..1043
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5935701"
 /issue_type="natural killer cells, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1b="NIH-MGC_106"
 /note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the

ORIGIN
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH-MGC Library."

Query Match 23.8%; Score 643; DB 5; Length 1043;
 Best Local Similarity 100.0%; Pred. No. 3.9e-269;
 Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 368 CTCATCATCTCCAGAGCCCTCCACCCAGAGAGTGGTGCATGTCTAGACACTGTC 427
 Db 1 CTCATCATCTCCAGAGCCCTCCACCCAGAGAGTGGTGCATGTCTAGACACTGTC 60
 QY 428 AAAGCTTAAGTCAACCATGAGTCTGACAGACATTAAGATGACCTGTGTGACCAATCT 487
 Db 61 AAAGCTTAAGTCAACCATGAGTCTGACAGACATTAAGATGACCTGTGTGACCAATCT 120
 QY 488 GACATGCTGCATGAGAACTGGGAAAGAGATGTGATTTATACCTTGAAAGCCCTGGGCA 547
 Db 121 GACATGCTGCATGAGAACTGGGAAAGAGATGTGATTTATACCTTGAAAGCCCTGGGCA 180
 QY 548 AGCACCATATGATGCTCCATTAATGAGTCCATCTCCCATCTCTCTGAGATGGGAGAAAG 607
 Db 181 AGCACCATATGATGCTCCATTAATGAGTCCATCTCTCTGAGATGGGAGAAAG 240
 QY 608 TGATATGACCTTCATCTGCTGAGTGGCAGAGAACCTGTGACAGAACTCTCAAGCCCAT 667
 Db 241 TGATATGACCTTCATCTGCTGAGTGGCAGAGAACCTGTGACAGAACTCTCAAGCCCAT 300
 QY 668 CTTGCCAGAGAACTCTGTGAAAGTGTGCTGATGACCCAGATTCCTCCATGCTCTCT 727
 Db 301 CTTGCCAGAGAACTCTGTGAAAGTGTGCTGATGACCCAGATTCCTCCATGCTCTCT 360
 QY 728 GTGTCTCTGTTGGTGGCCCTCTCTGCTCAGTCTCTTTTACTGGGGCTATTTCTTGGT 787
 Db 361 GTGTCTCTGTTGGTGGCCCTCTCTGCTCAGTCTCTTTTACTGGGGCTATTTCTTGGT 420
 QY 788 TCTGAAGAGAGAGACAGAAAGATGATTAAGAGAGAGAGATGAGATTTGTGCG 847
 Db 421 TCTGAAGAGAGAGACAGAAAGATGATTAAGAGAGAGAGATGAGATTTGTGCG 480
 QY 848 GGAAATCTCTTAACATATGCTCCCATCTTGTGAGAGAAACAGAGTACGACATCTCTCA 907
 Db 481 GGAAATCTCTTAACATATGCTCCCATCTTGTGAGAGAAACAGAGTACGACATCTCTCA 540
 QY 908 CACTAATGAACAAATCCCTAAAGAGATCCAGCAATACGGTTTCTCCACTGTGGAAT 967
 Db 541 CACTAATGAACAAATCCCTAAAGAGATCCAGCAATACGGTTTCTCCACTGTGGAAT 600
 QY 968 ACCGAAAAGATGAGAAATCCCACTCACTGCTCAGATGCCA 1010
 Db 601 ACCGAAAAGATGAGAAATCCCACTCACTGCTCAGATGCCA 643

RESULT 10
 B0712547 904 bp mRNA linear EST 16-JUL-2002
 LOCUS AGENCOURT_8501546 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6303158
 DEFINITION 5', mRNA sequence.
 ACCESSION B0712547
 VERSION B0712547.1 GI:21851446
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
<http://image.llnl.gov>
 Plate: LHC2521 row: m column: 15
 High quality sequence stop: 637.

FEATURES

SOURCE

Location/Qualifiers
 1. .904
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6103158"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_113"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GCCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match

23.4%; Score 632; DB 5; Length 904;
 Best Local Similarity 100.0%; Pred. No. 2,5e-264;

Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

62 CCTCACCCTATCATATCTCTTGGAGCTCAGAGGGTGCAGACCTCTGGAGCCGTGAA 121

1 CCTCACCCTATCATATCTCTTGGAGCTCAGAGGGTGCAGACCTCTGGAGCCGTGAA 60

122 AGAGCTGTGGTTCGCTTGGTGGGCGGTGACTTTCCCTGAAAGTCAAGTAAAGCA 181

61 AGAGCTGTGGTTCGCTTGGTGGGCGGTGACTTTCCCTGAAAGTCAAGTAAAGCA 120

182 AGTTGACTCTATTGTCTGAGACCTTCAACACACCCCTCTTGTCTACCATACCAAGCA 241

121 AGTTGACTCTATTGTCTGAGACCTTCAACACACCCCTCTTGTCTACCATACCAAGCA 180

242 GGGCACTATATGTGAGCCCAAAATCGTAATAGGAGAGATAGTATCCAGATGAGG 301

181 GGGCACTATATGTGAGCCCAAAATCGTAATAGGAGAGATAGTATCCAGATGAGG 240

302 CTACTCCCTGAAGCTCAGAACTGAAGAAATGATCTCAGGATCTTACTATGTGGGAT 361

241 CTACTCCCTGAAGCTCAGAACTGAAGAAATGATCTCAGGATCTTACTATGTGGGAT 300

362 ATACAGCTCATCTACTCCAGACCCCTCCACCAGAGATAGTGTGATCTTACAGCA 421

301 ATACAGCTCATCTACTCCAGACCCCTCCACCAGAGATAGTGTGATCTTACAGCA 360

422 CCGTCAAGCTTAAGTCAACATGGGTCTGAGAGAAATAGATGACCTGTGTGAC 481

361 CCGTCAAGCTTAAGTCAACATGGGTCTGAGAGAAATAGATGACCTGTGTGAC 420

482 CAATCTGACATGTGTCAGAACTAGGGAAGATGTGATTATATCTGGAAGCCCT 541

421 CAATCTGACATGTGTCAGAACTAGGGAAGATGTGATTATATCTGGAAGCCCT 480

542 GGGGCAAGCAGCCCAATAGTCCCATTAATGGGTCCATCTCTCTGAGATGGG 601

481 GGGGCAAGCAGCCCAATAGTCCCATTAATGGGTCCATCTCTCTGAGATGGG 540

602 AGAAGATATATGATCTTCAATCTGCGTTCAGAGAACCTCTCAGCAAACTTCTGAG 661

541 AGAAGATATATGATCTTCAATCTGCGTTCAGAGAACCTCTCTCAGCAAACTTCTGAG 600

662 CCCCATCTTGCAGGAAGCTCTGTGAAGTG 693

Db 601 CCCCATCTTGCAGGAAGCTCTGTGAAGTG 632

RESULT 11

BE326659/c

LOCUS

DEFINITION

BE326659 593 bp mRNA linear EST 14-JUL-2000
 hre2h10.x1 NCI CGAP Kid11 Homo sapiens CDNA clone IMAGE:313123 3'
 similar to TR:015430 015430 LEUCOCYTE ANTIGEN CD84. ;, mRNA
 sequence.

ACCESSION

BE326659 GI:9200435

VERSION

BE326659.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-rc@mail.nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL, send email to:
info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 449.
 Location/Qualifiers
 1. .593
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3133123"
 /lab_host="DH10B"
 /clone_id="NCI CGAP Kid11"
 /note="Organ: Kidney; Vector: pRTT3D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 Plasmid DNA from the normalized library NCI CGAP Kid1 was
 prepared, and 88 circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (cloneids 1322376-1323911, 1456007-1456775, and
 1500552-1502855). Subtraction by Bento Soares and M.
 Felicia Bonaldo."

FEATURES

SOURCE

Location/Qualifiers
 1. .593
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3133123"
 /lab_host="DH10B"
 /clone_id="NCI CGAP Kid11"
 /note="Organ: Kidney; Vector: pRTT3D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 Plasmid DNA from the normalized library NCI CGAP Kid1 was
 prepared, and 88 circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (cloneids 1322376-1323911, 1456007-1456775, and
 1500552-1502855). Subtraction by Bento Soares and M.
 Felicia Bonaldo."

ORIGIN

Query Match

21.8%; Score 589; DB 2; Length 593;
 Best Local Similarity 100.0%; Pred. No. 1.5e-245;

Matches 589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

490 CATGCTGACATGAAACATGGGGAAGAGATGATTTATACCTTGAAAGCCCTTGAGGCAAG 549

589 CATGCTGACATGAAACATGGGGAAGAGATGATTTATACCTTGAAAGCCCTTGAGGCAAG 530

550 CAGCCATATGATGCCATTAATGGGTCCATCTCCCAATCTCTGAGATGGGGAAGAAAGTG 609

529 CAGCCATATGATGCCATTAATGGGTCCATCTCCCAATCTCTGAGATGGGGAAGAAAGTG 470

610 ATATGACCTTCATCTGCTGACAGAAACCTCTCAGCAGAACTTCTCAAGCCCATCC 669

469 ATATGACCTTCATCTGCTGACAGAAACCTCTCAGCAGAACTTCTCAAGCCCATCC 410

670 TTGCCAGAAAGCTCTGTGAAGGTGCTGCTGATGATCCAGATTCTCCATGCTCTCTGT 729

409 TTGCCAGAAAGCTCTGTGAAGGTGCTGCTGATGATCCAGATTCTCCATGCTCTCTGT 350

Oy	730	GTCTCCCTTGGTGGCCCTCCCTGCTGCACTCTCTTTGATCTGGGGCTATTTCTTTGGTTCC	789
Db	349	GTCTCCCTTGGTGGCCCTCCCTGCTGCACTCTCTTTGATCTGGGGCTATTTCTTTGGTTCC	290
Oy	790	TGAAGAGAGAGACAAGAGAGATACATTGAAGAGAGAGAGAGATGGACATTTGTGGG	849
Db	289	TGAAGAGAGAGACAAGAGAGATACATTGAAGAGAGAGAGAGAGATGGACATTTGTGGG	230
Oy	850	AAACTCTTACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACCAATTCCTTCA	909
Db	229	AAACTCTTACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACCAATTCCTTCA	170
Oy	910	CTATATGACAATCCTTAAGAGAAATCCAGAAATTAAGTTACTCCATCTGTGAATAC	969
Db	169	CTATATGACAATCCTTAAGAGAAATCCAGAAATTAAGTTACTCCATCTGTGAATAC	110
Oy	970	CGAAAAAGATGAAAAATCCCACTCACTGCTCACGATCCAGACACCAAGCTATTG	1029
Db	109	CGAAAAAGATGAAAAATCCCACTCACTGCTCACGATCCAGACACCAAGCTATTG	50
Db	1030	CCTATGAGAAATGTTATCTTACAGACAGATGCACTCCCTTAAGTCTTGCT	1078
Db	49	CCTATGAGAAATGTTATCTTACAGACAGATGCACTCCCTTAAGTCTTGCT	1
RESULT 12			
CN480770/c			
LOCUS	CN480770	702 bp	mRNA linear EST 05-AUG-2004
DEFINITION	UI-H-PT2-bj9-g-17-0-UI.s1 NCI CGAP PT2 Homo sapiens cDNA clone		
	UI-H-PT2-bj9-g-17-0-UI 3', mRNA sequence.		
ACCESSION	CN480770		
VERSION	CN480770.1	GI:46549624	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 702)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Daniela S. Gerhard, Ph.D.		
	Office of Cancer Genomics		
	National Cancer Institute / NIH		
	Bldg. 31 Rm10A07 Bethesda, MD 20892		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: Dr. Gary W. Hunninghake, U of I		
	cDNA library preparation: Dr. M. Bento Soares, University of Iowa		
	cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa		
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa		
	Clone Distribution: Distribution information can be found at		
	http://genome.uiowa.edu/distribution/cgap.html		
	Seq primer: M13 FORWARD		
	POLYA=Yes.		
FEATURES			
source	Location/Qualifiers		
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	/tissue_type="Alveolar Macrophage"		
	/dev_stage="Adult"		
	/lab_host="DH10B (Life Technologies)"		
	/clone_1lb="NCI CGAP PT2"		
	/note="Organ: Lung; Vector: pT7f3-Pac (Pharmacia) with a		
	modified polylinker; Site 1: EcoR I; Site 2: Not I;		
	NCI CGAP PT2 is a subcloned cDNA library constructed from		
	a pool of 81 RNA samples from Alveolar Macrophages		
	challenged with different treatments. The mRNA samples		
	were a mixture of these conditions (times refer to		
	incubations following isolation by bronchoalveolar lavage)		
	(some normal donor macrophages were cultured in some of		

the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; LPS 100 ng/ml, 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad. vector + LPS 3 hours; Ad. vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subcloned according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-PT2
TAG_SEQ=GGCCATGCGG"

ORIGIN

the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subcloned according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-P12
TAG_SEQ=GGCCATCGCG"

Query Match	21.2%	Score 573	DB 7	Length 702
Best Local Similarity	99.9%	Pred. No. 1.4e-238		
Matches 693	Conservative 0	Mismatches 0	Indels 1	Gaps 1
397	AGTACGAGCTGCATAGTCTACGAGCACCCTGTCAAGCCTAAAGTCAACCATGGGTCTGAGA	456		
702	AGTAGGTGCTCATAGTCTACGAGCACCCTGTCAAGCCTAAAGTCAACCATGGGTCTGAGA	643		
457	GCAATAGAGATGGCACTGTGTGACCAATCTGCATATGCTGATGGAAATGGGAAAGAG	516		
642	GCAATAGAGATGGCACTGTGTGACCAATCTGCATATGCTGATGGAAATGGGAAAGAG	583		
517	ATGATATTTATACCCGGAAGGCCCTGGGGGCAAGCAGCAATGAATGCCATATGGGTCCA	576		
582	ATGATATTTATACCTGGAGGCCCTGGGGGCAAGCAGCAATGAATGCCATATGGGTCCA	523		
577	T-CTCCCATCTCTGTGAGATGGGGAAGAAATATGATCACTTCATCTGCGTTCAGG	635		
522	TCCCTCCCATCTCTGTGAGATGGGGAAGAAATATGATCACTTCATCTGCGTTCAGG	463		
636	AACTCTGTGAGCAAGAACTTCTCAAGCCCATCTTGTGCAGGAAGCTCTGGAAGTCT	695		
462	AACTCTGTGAGCAAGAACTTCTCAAGCCCATCTTGTGCAGGAAGCTCTGGAAGTCT	403		
686	GCTATGACCGAGATTCCTCATGATGCTCTGTGTCTCCGTGTGGTACCCTCTGCTC	755		
402	GCTATGACCGAGATTCCTCATGATGCTCTGTGTCTCCGTGTGGTACCCTCTGCTC	343		
756	AGTCTCTTGTACTGGGGCTATTTCTTGTGTTTGTGAAGAGAGAGACAAGAAAGTAC	815		
342	AGTCTCTTGTACTGGGGCTATTTCTTGTGTTTGTGAAGAGAGAGACAAGAAAGTAC	283		
816	ATTGAAGAGAAAGAGATGACATTTGTGGGAAACTCCTATCATATGCCCCCATCT	875		
282	ATTGAAGAGAAAGAGATGACATTTGTGGGAAACTCCTATCATATGCCCCCATCT	223		
876	GGAGAGAACACAGAGTACGACACATCCCTCACACTAATAGAAATCTTAAAGAAAT	935		
222	GGAGAGAACACAGAGTACGACACATCCCTCACACTAATAGAAATCTTAAAGAAAT	163		
936	CCAGCAATATGAGTTTACTTCCACTGTGGAAATACCGAAAAAGATGAAATATCCCATCA	995		
162	CCAGCAATATGAGTTTACTTCCACTGTGGAAATACCGAAAAAGATGAAATATCCCATCA	103		
996	CTGCTACGATGACAGACACACAAAGGCTATTTGGCTATGGAATGTTATCTTACACACA	1055		
102	CTGCTACGATGACAGACACACAAAGGCTATTTGGCTATGGAATGTTATCTTACACACA	43		
1056	GTGCACTCCCTTAAGTCTCTGCTCAAAAAAAA 1089			
42	GTGCACTCCCTTAAGTCTCTGCTCAAAAAAAA 9			

RESULT 13
CD687842 648 bp mRNA linear EST 25-JUN-2003
LOCUS CD687842
DEFINITION EST4363 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD687842
VERSION CD687842.1 GI:32206062
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yzeng@gzsums.edu.cn.
Location/Qualifiers
1. 648
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/issue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN
Query Match 21.2%; Score 572; DB 6; Length 648;
Best Local Similarity 100.0%; Pred. No. 3.9e-238;
Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GAGAGCAATATGCTGTTCCCAACATGCTCACCCTCATATATCTTTGGACCTC 92
DB 77 GAGAGCAATATGCTGTTCCCAACATGCTCACCCTCATATATCTTTGGACCTC 136
QY 93 ACAGGCTCAGAGCTGAGCCCGTAAGAGCTGCTCGTTGGTGGGGCCGTG 152
DB 137 ACAGGCTCAGAGCTGAGCCCGTAAGAGCTGCTCGTTGGTGGGGCCGTG 196
QY 153 ACTTTCCCTGGAAGTCAAGTAAGCAAGTTGACTATATGCTGGACCTTCAACA 212
DB 197 ACTTTCCCTGGAAGTCAAGTAAGCAAGTTGACTATATGCTGGACCTTCAACA 256
QY 213 ACCCTCTTGTCAACCATACAGCCAGAAAGGGGCACTATCATAGTACCCTTAAT 272
DB 257 ACCCTCTTGTCAACCATACAGCCAGAAAGGGGCACTATCATAGTACCCTTAAT 316
QY 273 AGGAGAGATAGACTCCAGATGAGGCTACCTCCGTAAGCTCAGCAAACTGAAGA 332
DB 317 AGGAGAGATAGACTCCAGATGAGGCTACCTCCGTAAGCTCAGCAAACTGAAGA 376
QY 333 AATGACTCAGGAGTCTACTATGTTGGGATATACAGTCACTCCAGACCTTCAC 392
DB 377 AATGACTCAGGAGTCTACTATGTTGGGATATACAGTCACTCCAGACCTTCAC 436
QY 393 CAGAGTACGTGCTGCTACTACAGACCTCTCAAGCCTTAAGTACCATGAGTCT 452
DB 437 CAGAGTACGTGCTGCTACTACAGACCTCTCAAGCCTTAAGTACCATGAGTCT 496
QY 453 CAGAGCAATAGATGAGCACTGTGTGCAATCTGCACTGCAAGCAATGGGAA 512
DB 497 CAGAGCAATAGATGAGCACTGTGTGCAATCTGCACTGCAAGCAATGGGAA 556
QY 513 GAGAGTGTGATTTATACCTGGAAGCCCTGGGCAAGCAATGATGCTCAATATGG 572

Db 557 GAGAGTGTGATTTATACCTGGAAGCCCTGGGCAAGCAATGATGCTCAATATGG 616
QY 573 TCCATCTCTCCCATCTCTGAGATGGGGA 604
DB 617 TCCATCTCTCCCATCTCTGAGATGGGGA 648

RESULT 14
AI638519/c 602 bp mRNA linear EST 14-DEC-1999
LOCUS AI638519/c
DEFINITION t08f02.x1 NCI_GCAP_GC6 Homo sapiens cDNA clone IMAGE:2240187 3', mRNA sequence.
ACCESSION AI638519
VERSION AI638519.1 GI:4690753
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS NCI-GCAP http://www.ncbi.nlm.nih.gov/ncigap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Straubeberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www.bio.lnl.gov/db/tp/image/image.html
Insert length: 840 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 462.
Location/Qualifiers
1. 602
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/clone="IMAGE:2240187"
/issue_type="pooled germ cell tumors"
/lab_note="DH10B"
/note="Vector: pTR3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_GCAP_GC4 was prepared, and 88 clones were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1257096-1258631, 1469064-1470983, and 1475992-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 21.0%; Score 567; DB 1; Length 602;
Best Local Similarity 100.0%; Pred. No. 6e-226;
Matches 567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1444 ATTATACCAAGTCTTGTCTACAGAGGGCAAGAACCAAAACAGACAGCAAGTCCA 1503
DB 594 ATTATACCAAGTCTTGTCTACAGAGGGCAAGAACCAAAACAGACAGCAAGTCCA 535
QY 1504 GCAGAGCAGATGACCTGCAAAATGATGATTAATTGGCTCTATAAATGATGGC 1563
DB 534 GCAGAGCAGATGACCTGCAAAATGATGATTAATTGGCTCTATAAATGATGGC 475
QY 1564 CAGACATATGCTGAGCTTACATTAATTGTCAGACCTGCTGCTCATGAAATTTGG 1623
DB 474 CAGACATATGCTGAGCTTACATTAATTGTCAGACCTGCTGCTCATGAAATTTGG 415

QY	1624	TTCCAAATGAATGAAC	CTATTCTTCATGAGACAGT	TTGAGACAGGCT	TGACCAACAGAT	TTCCAG	1683
Db	414	CTCCAAATGAATGAAC <td>CTACTCTTTCATGAGACAGT <th>TTGAGACAGGCT</th> <th>TGACCAACAGAT</th> <th>TTCCAG</th> <th>355</th> </td>	CTACTCTTTCATGAGACAGT <th>TTGAGACAGGCT</th> <th>TGACCAACAGAT</th> <th>TTCCAG</th> <th>355</th>	TTGAGACAGGCT	TGACCAACAGAT	TTCCAG	355
QY	1684	AGGGCCAGGTGTGAT <td>CCACAGAGACTT <td>TGAAGGTCAAAGT <td>TTCACAAAGATGAAGAT <td>CAGG</td> <td>1743</td> </td></td></td>	CCACAGAGACTT <td>TGAAGGTCAAAGT <td>TTCACAAAGATGAAGAT <td>CAGG</td> <td>1743</td> </td></td>	TGAAGGTCAAAGT <td>TTCACAAAGATGAAGAT <td>CAGG</td> <td>1743</td> </td>	TTCACAAAGATGAAGAT <td>CAGG</td> <td>1743</td>	CAGG	1743
Db	354	AGGGCCAGGTGTGAT <td>CCACAGAGACTT <td>TGAAGGTCAAAGT <td>TTCACAAAGATGAAGAT <td>CAGG</td> <td>295</td> </td></td></td>	CCACAGAGACTT <td>TGAAGGTCAAAGT <td>TTCACAAAGATGAAGAT <td>CAGG</td> <td>295</td> </td></td>	TGAAGGTCAAAGT <td>TTCACAAAGATGAAGAT <td>CAGG</td> <td>295</td> </td>	TTCACAAAGATGAAGAT <td>CAGG</td> <td>295</td>	CAGG	295
QY	1744	GTAGCTGACCAT <td>GTTTGGCAGATAC <td>CTATTAATGAGACACAGAGT <td>GTGCATGCCCCAAGG</td> <td></td> <td>1803</td> </td></td>	GTTTGGCAGATAC <td>CTATTAATGAGACACAGAGT <td>GTGCATGCCCCAAGG</td> <td></td> <td>1803</td> </td>	CTATTAATGAGACACAGAGT <td>GTGCATGCCCCAAGG</td> <td></td> <td>1803</td>	GTGCATGCCCCAAGG		1803
Db	294	GTAGCTGACCAT <td>GTTTGGCAGATAC <td>CTATTAATGAGACACAGAGT <td>GTGCATGCCCCAAGG</td> <td></td> <td>235</td> </td></td>	GTTTGGCAGATAC <td>CTATTAATGAGACACAGAGT <td>GTGCATGCCCCAAGG</td> <td></td> <td>235</td> </td>	CTATTAATGAGACACAGAGT <td>GTGCATGCCCCAAGG</td> <td></td> <td>235</td>	GTGCATGCCCCAAGG		235
QY	1804	ACAAAGACCTCCAGC <td>CAGGCTTCATTTATGCACT <td>TTGTGCTGCTCAAAAGAAAGT <td>CTAGAGTT</td> <td></td> <td>1863</td> </td></td>	CAGGCTTCATTTATGCACT <td>TTGTGCTGCTCAAAAGAAAGT <td>CTAGAGTT</td> <td></td> <td>1863</td> </td>	TTGTGCTGCTCAAAAGAAAGT <td>CTAGAGTT</td> <td></td> <td>1863</td>	CTAGAGTT		1863
Db	234	ACAAAGACCTCCAGC <td>CAGGCTTCATTTATGCACT <td>TTGTGCTGCTCAAAAGAAAGT <td>CTAGAGTT</td> <td></td> <td>175</td> </td></td>	CAGGCTTCATTTATGCACT <td>TTGTGCTGCTCAAAAGAAAGT <td>CTAGAGTT</td> <td></td> <td>175</td> </td>	TTGTGCTGCTCAAAAGAAAGT <td>CTAGAGTT</td> <td></td> <td>175</td>	CTAGAGTT		175
QY	1864	TTAAGGCTGTGTC <td>CAGAACCCATCCCAATAAAGAGACG <td>AGTCTGAAATGACATTTGTAAT</td> <td></td> <td></td> <td>1923</td> </td>	CAGAACCCATCCCAATAAAGAGACG <td>AGTCTGAAATGACATTTGTAAT</td> <td></td> <td></td> <td>1923</td>	AGTCTGAAATGACATTTGTAAT			1923
Db	174	TTAAGGCTGTGTC <td>CAGAACCCATCCCAATAAAGAGACG <td>AGTCTGAAATGACATTTGTAAT</td> <td></td> <td></td> <td>115</td> </td>	CAGAACCCATCCCAATAAAGAGACG <td>AGTCTGAAATGACATTTGTAAT</td> <td></td> <td></td> <td>115</td>	AGTCTGAAATGACATTTGTAAT			115
QY	1924	CTAGTGTAGAGACT <td>TGGAGTTCAGGCACTGATGAGACT <td>GTGTGGGCAACGGGGGGCAGTGGGTA</td> <td></td> <td></td> <td>1983</td> </td>	TGGAGTTCAGGCACTGATGAGACT <td>GTGTGGGCAACGGGGGGCAGTGGGTA</td> <td></td> <td></td> <td>1983</td>	GTGTGGGCAACGGGGGGCAGTGGGTA			1983
Db	114	CTAGTGTAGAGACT <td>TGGAGTTCAGGCACTGATGAGACT <td>GTGTGGGCAACGGGGGGCAGTGGGTA</td> <td></td> <td></td> <td>55</td> </td>	TGGAGTTCAGGCACTGATGAGACT <td>GTGTGGGCAACGGGGGGCAGTGGGTA</td> <td></td> <td></td> <td>55</td>	GTGTGGGCAACGGGGGGCAGTGGGTA			55
QY	1984	CTTGTAACCTTTAAAGAT <td>TGTTAATT</td> <td>2010</td> <td></td> <td></td> <td></td>	TGTTAATT	2010			
Db	54	CTTGTAACCTTTAAAGAT <td>TGTTAATT</td> <td>28</td> <td></td> <td></td> <td></td>	TGTTAATT	28			
RESULT 15							
LOCUS	B1767020						
DEFINITION	B1767020	920 bp	mRNA	linear	EST 25-SEP-2001		
ACCESSION	603054228F1	NIH_MGC_122	Homo sapiens	cDNA clone IMAGE:5203638	5',		
VERSION	B1767020						
KEYWORDS	B1767020.1	GI:15758598					
SOURCE	EST.						
ORGANISM	Homo sapiens (human)						
REFERENCE	Homo sapiens						
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.						
JOURNAL	1 (bases 1 to 920)						
COMMENT	NIH-MGC http://mgs.nci.nih.gov/.						
	National Institutes of Health, Mammalian Gene Collection (MGC)						
	Unpublished (1999)						
	Contact: Robert Strausberg, Ph.D.						
	Email: cgaabse-remail.nih.gov						
	Tissue Procurement: Life Technologies, Inc.						
	cDNA Library Preparation: Life Technologies, Inc.						
	cDNA Sequencing by: Incyte Genomics, Inc.						
	Clone distribution: MGC clone distribution information can be						
	found through the I.M.A.G.E. Consortium/BLNI at:						
	http://image.llnl.gov						
	Plate: L1M11510	row: h	column: 07				
FEATURES	High quality sequence stop: 743.						
source	Location/Qualifiers						
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5203638"
/lab_host="DH10B"
/clone_id="NH1.MGC.122"
/note="Organ: pooled lung and spleen; Vector: pCMV-Sport6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source:
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber

```

(Invitrogen). Research Genetics tracking code 026. Note this is a NIH_MGC Library."

Query Match	20.3%	Score 550	DB 4	Length 920
Best Local Similarity	99.7%	Pred. No.	1.5e-228	
Matches 720	Conservative	0	Mismatches 1	Indels 1
				Gaps 1

QY	31	CAGAGAGCAATATGAGTGGTTCCCAACATGCTCAACCCATCATATATCTCTTTGGCAGC	90
Db	1	CAGAGAGCAATATGAGTGGTTCCCAACATGCTCAACCCATCATATATCTCTTTGGCAGC	60
QY	91	TCACAGGGTCAGCAGCCTCTTGGAACCCGTGAAGAGCTGATGGTTCCGTGGTGGGGCCG	150
Db	61	TCACAGGGTCAGCAGCCTCTTGGAACCCGTGAAGAGCTGATGGTTCCGTGGTGGGGCCG	120
QY	151	TGACTTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTATATGTCTGCAACCTTCAACA	210
Db	121	TGACTTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTATATGTCTGCAACCTTCAACA	180
QY	211	CAACCCCTCTTGTCAACATACAGCCAGAGGGGGCACTATCATATAGTGAACCCAAAATCGTA	270
Db	181	CAACCCCTCTTGTCAACATACAGCCAGAGGGGGCACTATCATATAGTGAACCCAAAATCGTA	240
QY	271	ATAGGGAGAGTGAATTCCTCCCAATGGAAGGCTACTCCCTGAAGTACAGCAAACTGAAGA	330
Db	241	ATAGGGAGAGTGAATTCCTCCCAATGGAAGGCTACTCCCTGAAGTACAGCAAACTGAAGA	300
QY	331	AGAATGACTCAGGAGATCTATATGTGGGGATATACAGCTCATCACTCAGAGCCCTCCA	390
Db	301	AGAATGACTCAGGATCTATATGTGGGGATATACAGCTCATCACTCAGAGCCCTCCA	360
QY	391	CCAGAGATACGTGCTGATGTCTACAGACACTGTCAAAGCCTTAAATCAACATGGGTC	450
Db	361	CCAGAGATACGTGCTGATGTCTACAGACACTGTCAAAGCCTTAAATCAACATGGGTC	420
QY	451	TGCAGAGCAATAAATGCGACCTGTGTGACCATCTGACATGTGCGATGGAACAATGGGG	510
Db	421	TGCAGAGCAATAAATGCGACCTGTGTGACCATCTGACATGTGCGATGGAACAATGGGG	480
QY	511	AAGAGGATGTTATTTATPACTTGGAAGGCCCTGTGGGGCAAGCAGCAATGATCCCATATATG	570
Db	481	AAGAGGATGTTATTTATPACTTGGAAGGCCCTGTGGGGCAAGCAGCAATGATCCCATATATG	540
QY	571	GGTCCATCTCTCCCATCTCTCGAGATGGGGA-GAAAGTATATGACTTCACTCTGCGTT	629
Db	541	GGTCCATCTCTCCCATCTCTCGAGATGGGGA-GAAAGTATATGACTTCACTCTGCGTT	600
QY	630	GCCAGGAACCTGTACAGAGAACTTCTCAAGCCCAACCTTATGCGAGGAACCTCTGTGA	689
Db	601	GCCAGGAACCTGTACAGAGAACTTCTCAAGCCCAACCTTATGCGAGGAACCTCTGTGA	660
QY	690	GGTCTGTGTATGACCAAGATTCCTCATATGATCTCTGTGTCTCTGTGGTGGCCCTC	749
Db	661	GGTCTGTGTATGACCAAGATTCCTCATATGATCTCTGTGTCTCTGTGGTGGCCCTC	720
QY	750	CT 751	
Db	721	CT 722	

RESULT 16	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
CB956896	760 bp	AGENCOURT 13178830 NIH MGC 164 Homo sapiens CDNA clone IMAGE:30351632 5', mRNA sequence.	CB956896			EST. CB956896.1 GI:30213013	Homo sapiens (human)
	mRNA	linear					Homo sapiens
							Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.


```

QY 866 CCCCCATTGTGAGAGACAGAGTACGACCAATCCCTCAGACTATATAGAAATCTCT 925
DB 463 CCCCCATTGTGAGAGACAGAGTACGACCAATCCCTCAGACTATATAGAAATCTCT 404
QY 926 AAGGAAAGATCCAGCAATACGTTTACTCTCACTGTGAAATTCGAAAAAAGATGAAAA 985
DB 403 AAGGAAAGATCCAGCAATACGTTTACTCTCACTGTGAAATTCGAAAAAAGATGAAAA 344
QY 986 TCCCCACTAGTCTCAGCAGTGCAGACACACCAAGGCTATTGCTATGAGAAATGTAT 1045
DB 343 TCCCCACTAGTCTCAGCAGTGCAGACACACCAAGGCTATTGCTATGAGAAATGTAT 284
QY 1046 CTAGACAGAGTGCAGTCTCCCTTAAGTCTGTCTCAAAAAAACAATTCGCGCCAAA 1105
DB 283 CTAGACAGAGTGCAGTCTCCCTTAAGTCTGTCTCAAAAAAACAATTCGCGCCAAA 224
QY 1106 GAAAAAATCAAGAAATTCAGTATTTGATTTGAAACATCAAGAGAAATGAAAGCT 1165
DB 223 GAAAAAATCAAGAAATTCAGTATTTGATTTGAAACATCAAGAGAAATGAAAGCT 164
QY 1166 TGACTTTTCCAGATTAATTATCTGTATGCTTTTAAAGATTAAAGTTGTAATTC 1225
DB 163 TGACTTTTCCAGATTAATTATCTGTATGCTTTTAAAGATTAAAGTTGTAATTC 104
QY 1226 CATCCACTGCTGAGAAATCTCTCAAAACCCAGAGGTTTAATCATCTTCAATCCCAAAAAG 1285
DB 103 CATCCACTGCTGAGAAATCTCTCAAAACCCAGAGGTTTAATCATCTTCAATCCCAAAAAG 44
QY 1286 GGATTGTGATGTCAAGCAAAACCTTAATAAAGTCTTAAGAT 1328
DB 43 GGATTGTGATGTCAAGCAAAACCTTAATAAAGTCTTAAGAT 1

RESULT 18
CD366944/c 739 bp mRNA linear EST 05-AUG-2004
LOCUS UI-H-FT2-bjp-1-06-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone
DEFINITION UI-H-FT2-bjp-1-06-0-UI 3', mRNA sequence.
ACCESSION CD366944
VERSION CD366944.1 GI:31151034
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 739)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source
Location/Qualifiers
1..739
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="UI-H-FT2-bjp-1-06-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10b (Life Technologies)"
/clone_1lb="NCI CGAP FT2"
/note="Organ: Lung; Vector: pT73-Pec (Pharmacia) with a
modified polylinker; Site_1: Ecor I; Site_2: Not I;
NCI CGAP FT2 is a subtracted cDNA library constructed from

```

ORIGIN

a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The RNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The RNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

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QY 414 TAGAGCAGCTGTCAAGCTTAAGTCAACCATGAGTGTGACAGAGCAATTAAGTGGACC 473
DB 684 TAGAGCAGCTGTCAAGCTTAAGTCAACCATGAGTGTGACAGAGCAATTAAGTGGACC 625
QY 474 TGTGTGACCAATCTGATGATGATGAAATGAGGAAAGATGATTTATACCTGG 533
DB 624 TGTGTGACCAATCTGATGATGATGAAATGAGGAAAGATGATTTATACCTGG 565
QY 534 AAGGCCCTGTGGGCAAGCAGCAATGATGATGATGATGATGATGATGATGATGATGATG 593
DB 564 AAGGCCCTGTGGGCAAGCAGCAATGATGATGATGATGATGATGATGATGATGATGATG 505
QY 594 AGATGGGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 653
DB 504 AGATGGGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 445
QY 654 TTCTCAAGCCCATCTCTTCCAGAAAGCTCTGTGAAGGTCGTGATGATGATGATGATG 713
DB 444 TTCTCAAGCCCATCTCTTCCAGAAAGCTCTGTGAAGGTCGTGATGATGATGATGATG 385
QY 714 TCCATGATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 773
DB 384 TCCATGATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 325
QY 774 CTATTTCTTTGTTTCTGAAGAGAGAGACAAAGAGTACATTGAAGAGAGAGAGAGAG 833
DB 324 CTATTTCTTTGTTTCTGAAGAGAGAGACAAAGAGTACATTGAAGAGAGAGAGAGAG 265
QY 834 GTGACATTTGTGCGGAAACTCTTAACATATGCCCCCATCTCTGAGAGAGAGAGAGAG 893
DB 264 GTGACATTTGTGCGGAAACTCTTAACATATGCCCCCATCTCTGAGAGAGAGAGAGAG 205
QY 894 GACACATCCCTCACACTTAATGAACAATCTTAAGAGAAATCCAGCAATACGTTTAC 953
DB 204 GACACATCCCTCACACTTAATGAACAATCTTAAGAGAAATCCAGCAATACGTTTAC 145
QY 954 TCCACTGTGAAATACGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGAC 1013
DB 144 TCCACTGTGAAATACGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGAC 85
QY 1014 ACACCAAGGCTATTTGCTTATGAGATGT 1042
DB 84 ACACCAAGGCTATTTGCTTATGAGATGT 56

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RESULT 19
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LOCUS AGENCOURT_14356154 NIH_MGC_191 Homo sapiens cDNA clone
DEFINITION IMAGE:30413029 5', mRNA sequence.
ACCESSION CD520950
VERSION CD520950.1 GI:31452668
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 842)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabds-remail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Narayan Bhat
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: NDCM207 row: f column: 14
High quality sequence stop: 464.
Location/Qualifiers
1. .842
/organism="Homo sapiens"
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/clone="IMAGE:30413029"
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/clone_id="NIH_MGC_191"
/note="Vector: pDNR-Lib; Site 1: SfiI (ggccatctggcc);
Site 2: SfiI (ggccgctggcc); Library is oligo-dT primed
and directionally cloned. PBMC - Peripheral Blood
Mononuclear Cells. RNA was pooled from 3/6hour stimulation
with PMA and Ionomycin. 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGCCATATGACC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGGCGGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 19.2%; Score 519; DB 6; Length 842;
Best Local Similarity 99.8%; Pred. No. 5e-215;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

25 GACTTCAGAGAGCAATATGCTGTTCCCAACATGCTCACCTCATATATCTT 84
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Db 5 GACTTCAGAGAGCAATATGCTGTTCCCAACATGCTCACCTCATATATCTT 64
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Qy 85 GGCAGCTCACAGGGTTCAGACCTCTGAGACCCGTGAAGAAGAGCTGTCGTTCCGTTG 144
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Db 65 GGCAGCTCACAGGGTTCAGACCTCTGAGACCCGTGAAGAAGAGCTGTCGTTG 124
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Qy 145 GGGCGGTGACTTTCCCTCTGAATGCCAAGTAAAGCAAGTTGACTTATTTCTGACCT 204
|||||
Db 125 GGGCGGTGACTTTCCCTCTGAATGCCAAGTAAAGCAAGTTGACTTATTTCTGACCT 184
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Qy 205 TCACACACCCCTCTTGTCACTATACGACGAGAAAGGGGACATATCATGTGACCCAA 264
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Db 185 TCACACACCCCTCTTGTCACTATACGACGAGAAAGGGGACATATCATGTGACCCAA 244
|||||

Qy 265 ATGCTAATAGGAGAGAGTGTGACTTCCAGATGAGAGCTACTCCCTGAAGCTACGACAA 324
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Db 245 ATGCTAATAGGAGAGAGTGTGACTTCCAGATGAGAGCTACTCCCTGAAGCTACGACAA 304
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Qy 325 TGAAGAAGATGATCTAGGGATCTACTATGTTGGGGATATACAGTCTACATCTCAGCAG 384
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Db 305 TGAAGAAGATGATCTAGGGATCTACTATGTTGGGGATATACAGTCTACATCTCAGCAG 364
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Qy 385 CTTCACCCAGAGATAGTCTGCTCATGTCTACAGACACCTGTCAAAAGCTTAAAGTACCA 444
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Db 365 CTTCACCCAGAGATAGTCTGCTCATGTCTACAGACACCTGTCAAAAGCTTAAAGTACCA 424
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Qy 445 TGGGTCTGACAGACATAGAAATGACCACTGTGTGACCAATCTGACATGCTGATGAA 504
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Db 425 TGGGTCTGACAGACATAGAAATGACCACTGTGTGACCAATCTGACATGCTGATGAA 484
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Qy 505 ATGGGAGAGAGATGTGATTATACCTGGAAGGCCCTGGGGCAAGCAGCAATGAGTCCC 564
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Db 485 ATGGGAGAGAGATGTGATTATACCTGGAAGGCCCTGGGGCAAGCAGCAATGAGTCCC 544
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Qy 565 ATATGGGTCCATCTCCCATCTCTGGA 594
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Db 545 ATATGGGTCCATCTCCCATCTCTGGA 574
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RESULT 20
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LOCUS AGENCOURT_6420769 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5541322
DEFINITION 5', mRNA sequence.
ACCESSION BM800975
VERSION BM800975.1 GI:19117798
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 1050)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM12238 row: n column: 11
High quality sequence stop: 584.
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/clone="IMAGE:5541322"
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/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 19.0%; Score 515; DB 4; Length 1050;
Best Local Similarity 99.8%; Pred. No. 2.7e-213;
Matches 565; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	417	TAGCACCTGTCAAAACCTTAAAGTCAACATGGGTCTGCAGAGCAATPAAGATGCAACCTGT	476
Db	51	GAGCACCTGTCAAAACCTTAAAGTCAACATGGGTCTGCAGAGCAATPAAGATGCAACCTGT	110
QY	477	GTGACCAATCTGCACATGTGTGCATGTGAACATGGGGAGAAAGAGATGTGATTTAATACCTGGAAG	536
Db	111	GTGACCAATCTGCACATGTGTGCATGTGAACATGGGGAGAAAGAGATGTGATTTAATACCTGGAAG	170
QY	537	GCCCTGGGGCAAGCAGCCCAATGATGCCCATTAATGGGTCCATCTCCCATCTCTTGAGAGA	596
Db	171	GCCCTGGGGCAAGCAGCCCAATGATGCCCATTAATGGGTCCATCTCCCATCTCTTGAGAGA	230
QY	597	TGGGAGAGAAATGATATATACCTTCACTTGGCGTTGCAGAGAAACCTGTACAGAGAAACTTC	656
Db	231	TGGGAGAGAAATGATATATACCTTCACTTGGCGTTGCAGAGAAACCTGTACAGAGAAACTTC	290
QY	657	TCAAGCCCCCATCTCTTGCAGAGAGCTCTGTGAAGGTGTGCTGATGATGACCCAGATTCTCC	716
Db	291	TCAAGCCCCCATCTCTTGCAGAGAGCTCTGTGAAGGTGTGCTGATGATGACCCAGATTCTCC	350
QY	717	ATGTCCTCTCTGTGTCTCTCTGTGGTGCCTCTCGTCAAGTCTCTTGTGTACTGGAGCTTA	776
Db	351	ATGTCCTCTCTGTGTCTCTCTGTGGTGCCTCTCGTCAAGTCTCTTGTGTACTGGAGCTTA	410
QY	777	TTTCTTTGGTTTCTTAAGAGAGAGACAAGAAAGTACATTGAAGAGAAAGAGAGATG	836
Db	411	TTTCTTTGGTTTCTTAAGAGAGAGACAAGAAAGTACATTGAAGAGAAAGAGAGATG	470
QY	837	GACATTTGTGGGAAACTCTTAACATATGCCCCCATTTCTGAGAGAGAACACAGATGACAG	896
Db	471	GACATTTGTGGGAAACTCTTAACATATGCCCCCATTTCTGAGAGAGAACACAGATGACAG	530
QY	897	ACAATCCCTCACTACATAATAGAACATCTCTAAAGAGAGATCCAGCAATACGGTTTACTCC	956
Db	531	ACAATCCCTCACTACATAATAGAACATCTCTAAAGAGAGATCCAGCAATACGGTTTACTCC	590
QY	957	ACTGTGGAATATCCGAAAAAGATGGA	982
Db	591	ACTGTGGAATATCCGAAAAAGATGGA	616

RESULT 21	CD366908/c	785 bp	mRNA	linear	EST 05-AUG-2004
LOCUS	CD366908				
DEFINITION	UI-H-F12-bjp-a-22-0-UI.s1 NCI CGAP F12 Homo sapiens CDNA clone UI-H-F12-bjp-a-22-0-UI 3', mRNA sequence.				

SOURCE ORGANISM	Homo sapiens (human)
-----------------	----------------------

Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.

REFERENCE
AUTHORS
TITLE
NATIONAL CANCER INSTITUTE
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap/>
1 (bases 1 to 785)

JOURNAL
IMMUNE
TUMOR Gene Index
Immunobased (1997)
National Cancer Institute, cancer genome anatomy project (CGAP)

COMMENT Contact: Robert S

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.iowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=yes.

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/tissue_type="Alveolar Macrophage"
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/clone_id="NCI CGAP PT2"
/note="Organ: lung; Vector: pRTT3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP PT2 is a subcloned cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/mL, 3 hours; LPS 100 ng/mL, 24 hours;
PMA 10 ng/mL, 3 hours; PMA 10 ng/mL, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph
aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
The library was subcloned according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. The tissue
was provided by Dr. Gary W. Hunninghake of the University
of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_L1B=UI-H-PT2
TAG_SEQ=GGCCATGCGC"

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ORIGIN

Query Match	18.9%	Score 512;	DB 6;	Length 785;
Best Local Similarity	99.8%	Pred. No. 5,7e-212;		
Matches 562;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0

QY	527	TACCTGGAAAGGCCCTGGGGCAAGACGCCAAATGAGTCCCATATATGGATCATCTCCCAT	586
Db	571	TACCTGGAAAGGCCCTGGGGCAAGACGCCAAATGAGTCCCATATATGGATCATCTCCCAT	512
QY	587	CTCTGGAGATGGGGAGAAAGTATGATATGACCTTCACTCTGCTGGCAGAAACCTGTGAG	646
Db	511	CTCTGGAGATGGGGAGAAAGTATGATATGACCTTCACTCTGCTGGCAGAAACCTGTGAG	452
QY	647	CAGAAACTTTCAGGCCCATCTCTTGGCAGAGAACTCTGTGAAGGTGCTGCTGATGACCC	706
Db	451	CAGAAACTTTCAGGCCCATCTCTTGGCAGAGAACTCTGTGAAGGTGCTGCTGATGACCC	392
QY	707	AGATTCCCTCAGAGGTCCTGTGTCTCTGTGGTGGCCCTCGTCACTGCTCTTTGT	766
Db	391	AGATTCCCTCAGAGGTCCTGTGTCTCTGTGGTGGCCCTCGTCACTGCTCTTTGT	332
QY	767	ACTGGGGCTATTTCTTTGGTTCCTGAAGAGAGAGACAGAAAGATACATTGAAGAGA	826
Db	331	ACTGGGGCTATTTCTTTGGTTCCTGAAGAGAGAGACAGAAAGATACATTGAAGAGA	272
QY	827	GAAGAGATGACATTTGTGGGAAACCTCTTACATATGCCCCCATTTCTGAGAGAACAC	886
Db	271	GAAGAGATGACATTTGTGGGAAACCTCTTACATATGCCCCCATTTCTGAGAGAACAC	212
QY	887	AGAGTAGACACCAATTCCTCACTAATAGAAACATCTCTAAAGGAAGATCCAGCAATAC	946
Db	211	AGAGTAGACACCAATTCCTCACTAATAGAAACATCTCTAAAGGAAGATCCAGCAATAC	152
QY	947	GATTATCTCCACTGTGAAATACCGAAAGAGTGGAAATCCCACTCACTGCTCAGCAT	1000
Db	151	GATTATCTCCACTGTGAAATACCGAAAGAGTGGAAATCCCACTCACTGCTCAGCAT	92
QY	1007	GCCAGACACACCAAGGCTATTTGCTATGAGATTTATCTAGACAGATGCACTCCCC	1066

Db	534	CAAGGAGCCATGATGCCATTAATGGGTGCATCCTCCNCAATCTCTGGAGATGGGAGAA	475
Qy	606	AGTGAATGACCTTCATCTGGTTGCCAGAAACCTGTGCAGAAACTTCTCAAGCCCC	665
Db	474	AGTGAATGACCTTCATCTGGCTTCCAGGAAACCTGTGAGAGAACTTCTCAAGCCCC	415
Qy	666	ATCTTGCAGGAACCTCTGTGAAGGTGCTGTATGACCAGATTTCCATGGTCTC	725
Db	414	ATCTTGCAGGAACCTCTGTGAAGGTGCTGTATGACCAGATTTCTCATGGTCTC	355
Qy	726	CTGTCTCTCTGTTGTTGGCCCTCTGCTCAGTCTCTTTGTACTGGGCTATTTCTTTGG	785
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Qy	786	TTTCTGAGAGAGAGACAAGAAAGTACATTGAAGAAAGAAAGATGGACATTTGT	845
Db	294	TCTCTGAAGAGAGACAAGAAAGTACATTGAAGAAAGAAAGATGGACATTTGT	235
Qy	846	CGGGAACCTCTTAACATATGCCCATTTCTGAGAGAAACAAGATACGACATCCCT	905
Db	234	CGGGAACCTCTCTTAACATATGCCCATTTCTGAGAGAAACAAGATACGACATCCCT	175
Qy	906	CACCTAATTAAACAATCCTTAAGAAATCAGCAATTAAGGTTAATCTCACTGTGAA	965
Db	174	CACCTAATTAAACAATCCTTAAGAAATCAGCAATTAAGGTTAATCTCACTGTGAA	115
Qy	966	ATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGACACAAAGGCTA	1025
Db	114	ATACCGAAAAAGATGAAAAATCCCACTCACTGCTCAGATGCCAGACACAAAGGCTA	55
Qy	1026	TTTGCGTATGAAATGTTATCTAGAACAGATGCACTCCCTTAAGTCTCTGTC	1079
Db	54	TTTGCGTATGAAATGTTATCTAGAACAGATGCACTCCCTTAAGTCTCTGTC	1

RESULT	24
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LOCUS	
DEFINITION	BFO26131 980 bp mRNA linear EST 10-OCT-2000 6016699191 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3952876 5', mRNA sequence.
ACCESSION	BFO26131
VERSION	BFO26131.1 GI:10733843
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Eumetazoa; Euteheria; Primates; Carnivora; Hominiidae; Homo. 1 (bases 1 to 980) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
AUTHORS	Contact: Robert Strausberg, Ph.D.
JOURNAL	Email: cgapbs-r@mail.nih.gov
COMMENT	Tissue Procurement: ATCC/DCTD/DRP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: Image.lnl.gov Plate: LILCM823 row: e column: 05 High quality sequence set:650.

FEATURES

source

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note="Organ: skin; Vector: pOT7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'

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ORIGIN

Query Match	17.7%	Score 479;	DB 2;	Length 980;
Best Local Similarity	99.8%;	Pred. No. 1.4e-197;		
Matches 599;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1

QY	424	IGTCAAAAGCCCTAAAGTCAACATGGGTCTGCAGAGCAATAAGATGGCACTGTGTGACCA	483
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QY	484	ATCTGACATGCTGCATGGAAATGAGGAAAGATGTGATTTATACCTGGAAAGCCCTTG	543
Db	61	ATCTGACATGCTGCATGGAAATGAGGAAAGATGTGATTTATACCTGGAAAGCCCTTG	120
QY	544	GGCAAGCAGCCCAATGATGCCATATATGGGTCCATCTCTCCCATCTCTCTGGAGATGGGGAG	603
Db	121	GGCAAGCAGCCCAATGATGCCATATATGGGTCCATCTCTCCCATCTCTCTGGAGATGGGGAG	180
QY	604	AAAGTATGATGACCTTCATCTGCGTTGTCAGAGAACCTGTGCAGAGAACTCTCAAGCC	663
Db	181	AAAGTATGATGACCTTCATCTGCGTTGTCAGAGAACCTGTGCAGAGAACTCTCAAGCC	240
QY	664	CCATCTCTTGCAGGAAGCTCTGTGAAGGTGCTGTGATGATGACCCAGATTCCTTCATGTTC	723
Db	241	CCATCTCTTGCAGGAAGCTCTGTGAAGGTGCTGTGATGATGACCCAGATTCCTTCATGTTC	300
QY	724	TCTGTGTCTCTGTGTGGTGGCCCTCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTT	783
Db	301	TCTGTGTCTCTGTGTGGTGGCCCTCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTT	360
QY	784	GSTTTCTGAAGAGAGAGACAGAAGAGTCAATTGAAGAGAAGAGAGTGGACATT	843
Db	361	GSTTTCTGAAGAGAGAGACAGAAGAGTCAATTGAAGAGAAGAGAGTGGACATT	420
QY	844	GTGGGAAACTCTTAACATA-TGCCCCCATCTGTGAGAGAACACAGAATACACACAATC	902
Db	421	GTGGGAAACTCTTAACATA-TTGCCCCCATCTGTGAGAGAACACAGAATACACACAATC	480
QY	903	CCTCACTAATAGAACATCTTAAGAGAGATCCAGCAATACGGTTTACTCCACTGTG	962
Db	481	CCTCACTAATAGAACATCTTAAGAGAGATCCAGCAATATACGGTTTACTCCACTGTG	540
QY	963	GAATATCCGAAAAAGATGGAAAAATCCCACTCACTGCTCAGATGTCGACAGACACACAAG	1022
Db	541	GAATATCCGAAAAAGATGGAAAAATCCCACTCACTGCTCAGATGTCGACAGACACACAAG	600

RESULT	25
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LOCUS	AM293413
DEFINITION	UI-H-BI2-ah1.h-12-0-UI.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727407 3', mRNA sequence.
ACCESSION	AM293413
VERSION	AM293413.1 GI:6700049
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 534)	NCI-CCAP	http://www.ncbi.nlm.nih.gov/ncicgap .		
	National Cancer Institute,	Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index			
	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D.			

Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www.bio.lnl.gov/bdip/image/image.html
Seq primer: M13 Forward
POLYAyes.

FEATURES

Source

1. 534
/organism="Homo sapiens"
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/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Sub4"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NCI CGAP Sub4 library is a substracted library derived from the NCI CGAP Sub2 library which is a substracted library derived from the NCI CGAP Sub1 library, which is a substracted library derived from BI. Bi constitutes a mixture of 21 normalized or substracted NCI CGAP libraries: NCI CGAP Co4, NCI CGAP Pr22, NCI CGAP Pr28, NCI CGAP Kid12, NCI CGAP Kid3, NCI CGAP Kid5, NCI CGAP Lym2, NCI CGAP Br2, NCI CGAP Co8, NCI CGAP CLL1, NCI CGAP Lei2, NCI CGAP Br23, NCI CGAP Lu5, NCI CGAP Lu24, NCI CGAP Lu19, NCI CGAP GC4, NCI CGAP GC6, NCI CGAP Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:
NCI CGAP Kid3 pool 1 : LLM 3334-3337, 3682-3683, 3788-3803 (IMAGE Clonides 1322376-1323811, 1456008-1456775, 1500552-1502855) NCI CGAP Kid5 pool 1 : LLM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonides 1323912-1325831, 1471368-1472903, 1492104-1493355)
NCI CGAP Lu5 pool 1 : LLM 3575-3582, 3851-3854 (IMAGE Clonides 1414920-1417991, 1520904-1522439) NCI CGAP GC4 pool 1 : LLM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonides 1257096-1258631, 1469064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1 : LLM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonides 985608-986759, 1101197-1101959, 1217928-1220615) NCI CGAP Co10 pool 1 : LLM 2644-2653, 2871-2872 (IMAGE Clonides 1057416-1061255, 1144584-1145351) Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.]
TAG_TISSUE=germ cell
TAG_LIB=NCI CGAP_GC4
TAG_SEQ=AAATC"

ORIGIN

Query Match 17.3%; Score 467; DB 2; Length 534;
Best Local Similarity 99.8%; Pred. No. 2.5e-192;
Matches 517; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1521 TGACAAAATGATGATTAATGCTCTAATACTATGTCACGACATAGCTGAGCT 1580
534 TGACAAAATGATGATTAATGCTCTAATACTATGTCACGACATAGCTGAGCT 475
1581 TACACTAATGCTGACAGCTGCTGCTCCCTCATGAAATGGCTCCAAATGAATGA 1640
474 TACACTAATGCTGACAGCTGCTGCTCCCTCATGAAATGGCTCCAAATGAATGA 415
1641 ACTTCATGACAGCTGACAGCTGACACAGATTCACAGAGGCGAGGTGTGATC 1700
414 ACTTCATGACAGCTGACAGCTGACACAGATTCACAGAGGCGAGGTGTGATC 355
1701 CACAGAGCTTGAGAGTCAAAAGTTCACAAAGATGAAGATCAGGCTAGCTGACATGTTTG 1760
354 CACAGAGCTTGAGAGTCAAAAGTTCACAAAGATGAAGATCAGGCTAGCTGACATGTTTG 295

QY 1761 GCAGATCTATATGAGACACAGAAAGTGTGATGGCCCAAGACAGACCTCCAGCCA 1820
DB 294 GCAGATCTATATGAGACACAGAAAGTGTGATGGCCCAAGACAGACCTCCAGCCA 235
QY 1821 GGGTTCAATTTATGACCTGCTGTGCTGCAAAAAGAAAGTCTAGTTTAAAGCTGTGCCA 1880
DB 234 GGGTTCAATTTATGACCTGCTGTGCTGCAAAAAGAAAGTCTAGTTTAAAGCTGTGCCA 175
QY 1881 CCCATCCCAATTAAGAGACCCGAGTCTGAACTCATTTGTAATCTGTAGTGAAGACTTG 1940
DB 174 CCCATCCCAATTAAGAGACCCGAGTCTGAACTCATTTGTAATCTGTAGTGAAGACTTG 115
QY 1941 GAGTCAGGCGTAGAGCTGTGGGGGACCGGGGGGCACTGGGTCTTGTAAACCTTTAAAG 2000
DB 114 GAGTCAGGCGTAGAGCTGTGGGGGACCGGGGGGCACTGGGTCTTGTAAACCTTTAAAG 55
QY 2001 ATGTTAATTCATTCATAGATATTTTATTAAGAACCTTA 2038
DB 54 ATGTTAATTCATTCATAGATATTTTATTAAGAACCTTA 17

RESULT 26
AA921765/c 444 bp mRNA linear EST 23-JUN-1998
LOCUS 0M43611.61 Soares_NFL.T GBC.S1 Homo sapiens cDNA clone
DEFINITION IMAGE:1543844 3', mRNA sequence.
ACCESSION AA921765
VERSION AA921765.1 GI:3069074
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TUMOR Gene Index
JOURNAL
COMMENT Unpublished (1997)
Contact: Robert Straubeberg, Ph.D.
Email: cgaps@mail.nih.gov
This clone is available royalty-free through ILNL; contact the IMAGE Consortium (infoimage.lnl.gov) for further information.
Insert length: 1101 Std Error: 0.00
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 443.

FEATURES

source

1. 444
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1543844"
/lab_host="DH10B"
/clone_lib="Soares_NFL.T GBC.S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung Nhlh19w, testis NHT, and B-cell NCI CGAP GCBI) were mixed, and as circles were made in vitro. Following HAP purification, this DNA was used as a tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNA from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 16.3%; Score 442; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 2.1e-181;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

740 GGTGCCCTCTGCTCAAGTCTTGTGACTGGGCTATTCTTGTGTTCTGAAGAGA 799

Db 443 GGTGCCCCCTCTCTCAGTCTCTTTGTATCGGGGCAATTTCTTTGGTTTCTGAAGAGA 384
 QY 800 GAGACAGAAGAGTATCATTTGAAGAGAAGAGAGTGAACATTTGCGGAACTCTCTTA 859
 Db 383 GAGACAGAAGAGTATCATTTGAAGAGAAGAGAGTGAACATTTGCGGAACTCTCTTA 324
 QY 860 CATATGCCCCCATTTCTGAGAGAGACAGAGTACGACATTCCTCACAATAAGAAC 919
 Db 323 CATATGCCCCCATTTCTGAGAGAGACAGAGTACGACATTCCTCACAATAAGAAC 264
 QY 920 AATCCCTAAAGAGATTCAGCAATACGTTTCTCCTGTTGAAATACCGAAAGAT 979
 Db 263 AATCCCTAAAGAGATTCAGCAATACGTTTCTCCTGTTGAAATACCGAAAGAT 204
 QY 980 GGAATATCCCATCTCACTGCTCAGATGCGACACACACAGGCTATTTGCTATGAGA 1039
 Db 203 GGAATATCCCATCTCACTGCTCAGATGCGACACACACAGGCTATTTGCTATGAGA 144
 QY 1040 TGTATCTAGACAGACAGTGCATCTCCCTTAAGTCTGCTCAAAAAAACAATTCG 1099
 Db 143 TGTATCTAGACAGACAGTGCATCTCCCTTAAGTCTGCTCAAAAAAACAATTCG 84
 QY 1100 CCGAAGAAAACAATGAGAAGATTCATGATTTGCTAGAAACATCAAGAAAGATGA 1159
 Db 83 CCGAAGAAAACAATGAGAAGATTCATGATTTGCTAGAAACATCAAGAAAGATGA 24
 QY 1160 GAACGTTGACTTTTTCACAGA 1181
 Db 23 GAACGTTGACTTTTTCACAGA 2

RESULT 27
 BG413358/c 484 bp mRNA linear EST 13-MAR-2001
 LOCUS 7037612.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3576214 3'
 DEFINITION similar to TR:092178 092178 CD84 LEUKOCYTE ANTIGEN.; mRNA
 sequence.
 ACCESSION BG413358
 VERSION BG413358.1 GI:13318911
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 484)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bcr-rt@mail.nih.gov
 Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
 info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 479.
 Location/Qualifiers
 1. 484
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3576214"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Kid11"
 /note="Organ: kidney; Vector: pYT3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Plasmid DNA from the normalized library NCI_CGAP_Kid3 was

prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (cloneids 132376-132391, 1456007-1456775, and
 1500552-1502855). Subtraction by Bento Soares and M.
 Fatima Bernaldo. "

ORIGIN
 Query Match 16.0%; Score 433; DB 4; Length 484;
 Best Local Similarity 99.8%; Pred. No. 1.7e-177;
 Matches 483; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

596 ATGGGAGAGAAATGATATGACCTTCACTGCGTTGCCAGAAACCTGTACAGAACTT 655
 Db 484 ATGGGAGAGAAATGATATGACCTTCACTGCGTTGCCAGAAACCTGTACAGAACTT 425
 QY 656 CTCAGGCCCATCTCTTCCAGAGAACTCTGTAGAGAGTGTGTATGACCCAGATTCTTC 715
 Db 424 CTCAGGCCCATCTCTTCCAGAGAACTCTGTAGAGAGTGTGTATGACCCAGATTCTTA 365
 QY 716 CATGGTCTCTGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 775
 Db 364 CATGGTCTCTGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 305
 QY 776 ATTTCTTTGTTTCTGAAGAGAGAGACAGAGAGATGATGATGAGAGAGAGAGAGT 835
 Db 304 ATTTCTTTGTTTCTGAAGAGAGAGACAGAGAGATGATGATGAGAGAGAGAGAGT 245
 QY 836 GGACATTTTGTGGGAAATCTCTTAACATATGCCCCCATTTCTGAGAGAACACAGATAGA 895
 Db 244 GGACATTTTGTGGGAAATCTCTTAACATATGCCCCCATTTCTGAGAGAACACAGATAGA 185
 QY 896 CACATCTCCCTCACATTAATGAGAACATCTTAAGAGAGATCAGCAATATACGTTTACTC 955
 Db 184 CACATCTCCCTCACATTAATGAGAACATCTTAAGAGAGATCAGCAATATACGTTTACTC 125
 QY 956 CACTGTGGAATATCGGAAAGATGAGAAATCCCACTCACTGCTCAGAGTCCAGACAC 1015
 Db 124 CACTGTGGAATATCGGAAAGATGAGAAATCCCACTCACTGCTCAGAGTCCAGACAC 65
 QY 1016 ACCAAGGCTATTTGGCTATGAGAAATGATATCTAGACACAGTGCATCCCTCAATCTCT 1075
 Db 64 ACCAAGGCTATTTGGCTATGAGAAATGATATCTAGACACAGTGCATCCCTCAATCTCT 5
 QY 1076 GCTC 1079
 Db 4 GCTC 1

RESULT 28
 BE044439/c 630 bp mRNA linear EST 08-JUN-2000
 LOCUS h045e03.x1 Soares_NFL_T GBC_S1 Homo sapiens cDNA clone
 DEFINITION IMAGE:3040348 3' similar to TR:015430 015430 LEUKOCYTE ANTIGEN
 CD84.; mRNA sequence.
 ACCESSION BE044439
 VERSION BE044439.1 GI:8361492
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 630)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bcr-rt@mail.nih.gov
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40UP from Gibco

FEATURES High quality sequence stop: 433.

Location/Qualifiers

1. 630

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3040348"

/lab_host="DH10B"

/clone_lib="Soares_NFL_T_GBC_S1"

/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBH19, testis NBT, and B-cell NCI CGAP GCB1) were mixed, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Patricia Bonaldo."

ORIGIN

Query Match

15.9%; Score 430; DB 2; Length 630;

Best Local Similarity 99.8%; Pred. No. 3,4e-176; Matches 480; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

857 TAAATATGCCCCCATCTTGGAGAGAACACAGAGTACAGACATCCCTCACAATAAG 916

505 TAACATATGCCCCCATCTTGGAGAGAACACAGAGTACAGACATCCCTCACAATAAG 446

917 AACATCTTAAAGAGATCCAGCAATAGCTTACTCCACTGTGAAATACCGAAAA 976

445 AACATCTTAAAGAGATCCAGCAATAGCTTACTCCACTGTGAAATACCGAAAA 386

977 GATGAAATCCCACTCACTGCTCAGATGCCAGACACAAAGGCTATTGCTATGA 1036

385 GATGAAATCCCACTCACTGCTCAGATGCCAGACACAAAGGCTATTGCTATGA 326

1037 GAATGTTATCTAGACAGACAGTCACTCCCTTAAGTCTCTCTCAAAAAAACAATTC 1096

325 GAATGTTATCTAGACAGACAGTCACTCCCTTAAGTCTCTCTCAAAAAAACAATTC 266

1097 CGGCCCCAAGAAATCAATCAAGAAATTCATGATTTGATCAAAATCAAGAAAT 1156

265 CGGCCCCAAGAAATCAATCAAGAAATTCATGATTTGATCAAAATCAAGAAAT 206

1157 GAGAAAGCTGATCTTTTCCAGGATTAATATCTGATGCTCTTTAGATTAAAGAT 1216

205 GAGAAAGCTGATCTTTTCCAGGATTAATATCTGATGCTCTTTAGATTAAAGAT 146

1217 TCGTAATTCATCACTGCTGAGAAATCTCTCAAAACCAAGGTTTAATCACTTATC 1276

145 TCATTAATTCATCACTGCTGAGAAATCTCTCAAAACCAAGGTTTAATCACTTATC 86

1277 CCAAAATGAGATTTGATATGTCAGCAAAACATTAATAAAGTGTGTAAGTATTCAT 1336

85 CCAAAATGAGATTTGATATGTCAGCAAAACATTAATAAAGTGTGTAAGTATTCAT 26

1337 A 1337

25 A 25

RESULT 29

BG743877 846 bp mRNA linear EST 15-MAY-2001

LOCUS 68272263F1 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:4849374 5',

DEFINITION mRNA sequence.

ACCESSION BG743877

VERSION BG743877.1 GI:14054530

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 846)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabs@mail.nih.gov

Tissue Procurement: Dr. Daniel McVicar, DBS/NCI

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LNCM1688 row: 0 column: 07

High quality sequence stop: 782.

Location/Qualifiers

1. 846

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4849374"

/issue_type="natural killer cells, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_106"

/note="Organ: Blood; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match

15.6%; Score 421; DB 4; Length 846;

Best Local Similarity 99.4%; Pred. No. 2.8e-172; Matches 621; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

921 ATCTTAAGAGAGATCCAGCAATACGTTTACTCCAGTGGAAATACCGAAAGATG 980

15 ATCTTAAGAGAGATCCAGCAATACGTTTACTCCAGTGGAAATACCGAAAGATG 74

981 GAAATATCCCACTCACTGCTCAGATGCCAGACACAAAGGCTATTGCTATGAGAT 1040

75 GAAATATCCCACTCACTGCTCAGATGCCAGACACAAAGGCTATTGCTATGAGAT 134

1041 GTTATCTAGACAGACAGTCACTCCCTTAAGTCTGCTCAAAAAAACAATTCGGC 1100

135 GTTATCTAGACAGACAGTCACTCCCTTAAGTCTGCTCAAAAAAACAATTCGGC 194

1101 CCAAGAAATCAATCAAGAAATTCAGATTGACTAGAAACATCAAGAAATGAGG 1160

195 CCAAGAAATCAATCAAGAAATTCAGATTGACTAGAAACATCAAGAAATGAGG 254

1161 AACGTGATCTTTTCCAGAGTAATATCTGATGCTCTTTAGATTAAAGTTCGT 1220

255 AACGTGATCTTTTCCAGAGTAATATCTGATGCTCTTTAGATTAAAGTTCGT 314

1221 AATTCATCACTGCTGAGAAATCTCTCAAAACCAAGGTTTAATCACTTATCCAA 1280

315 AATTCATCACTGCTGAGAAATCTCTCAAAACCAAGGTTTAATCACTTATCCAA 374

1281 AATGAGATTTGAGATGTCAGCAAAACCATTAATAAAGTCTTAGAGATTTCTATGAA 1340

375 AATGAGATTTGAGATGTCAGCAAAACCATTAATAAAGTCTTAGAGATTTCTATGAA 434

1341 ATGTAATCAAGATTCACATATTATAGACAGCTGTTGTAATGATGCTCCAGGT 1400

435 ATGTAATCAAGATTCACATATTATTAAGACAGCTGTTGTAATGATGCTCCAGGT 494

QY 1401 CAGTGTCTGAGATTTTCATTCATCCAGAGGCTTGATGTCAGATTATACAGAGTCTT 1460
DB 495 CAGTGTCTGAGATTTTCATTCATCCAGAGGCTTGATGTCAGATTATACAGAGTCTG 554
QY 1461 GCTACAGAGAGGCGAAGAACCAAAACAGACAGACAGTCCGCGAAGACAGATGACCC 1520
DB 555 GCTACAGAGAGGCGAAGAACCAAAACAGACAGACAGTCCGCGAAGACAGATGACCC 614
QY 1521 TGACAAAAATGATGATTATATGG 1545
DB 615 TGACAAAAATGATGATTATATGG 639

RESULT 30
BU166292 876 bp mRNA linear EST 04-SEP-2002
LOCUS BU166292
DEFINITION AGENCOURT_7944604 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6148660
5', mRNA sequence.
ACCESSION BU166292
VERSION BU166292.1 GI:22680244
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
1 (bases 1 to 876)
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DC/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM13480 row: h column: 05
High quality sequence stop: 724.
Location/Qualifiers
1. 876
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6148660"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/lab_lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 15.4%; Score 416; DB 5; Length 876;
Best Local Similarity 99.3%; Pred. No. 4.2e-170;
Matches 726; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 947 GGTTAATCTCACTGTGGAATACCGAAAAAGATGAAAAATCCCACTCACTGTCAGAT 1006
DB 1 GGTTAATCTCACTGTGGAATACCGAAAAAGATGAAAAATCCCACTCACTGTCAGAT 60
QY 1007 GCCAGACACACCAAGGCTATTTGGCTATAGATGTATCTAGACAGAGTGCATCCGCC 1066
DB 61 GCCAGACACACCAAGGCTATTTGGCTATAGATGTATCTAGACAGAGTGCATCCGCC 120
QY 1067 TAAGTCTGCTCAAAAAAACAATTCGCGCCCAAGAAAAACAATCAGAGAATTTCA 1126
DB 121 TAAGTCTGCTC-AAAAAACAATTCGCGCCCAAGAAAAACAATCAGAGAATTTCA 179
QY 1127 CTGATTGACTAGAAATCAGAGAAATGAAGAACTTGACTTTTTCAGATTAAT 1186

DB 180 CTGATTGACTAGAAATCAGAGAAATGAAGAACTTGACTTTTTCAGATTAAT 239
QY 1187 TATCTGTAGTCTCTTAAGATTTTAAGAGTTGTAATTCATCCATCGCTGGAATCTC 1246
DB 240 TATCTGTAGTCTCTTAAGATTTTAAGAGTTGTAATTCATCCATCGCTGGAATCTC 299
QY 1247 CTCAAACCCAGAAAGTTTAATCACTTCATCCCAAAATGGATTGTGAATGTCACAAAC 1306
DB 300 CTCAAACCCAGAAAGTTTAATCACTTCATCCCAAAATGGATTGTGAATGTCACAAAC 359
QY 1307 CATAAAAAAGTCTTAAGAGTTTCTATAGAAATGTAAATGCAAGGTCACATATTA 1366
DB 360 CATAAAAAAGTCTTAAGAGTTTCTATAGAAATGTAAATGCAAGGTCACATATTA 419
QY 1367 ATGACAGCTGTTGATTATATGATGCTCCAGAGTGTGATGATTTTCATTCATCC 1426
DB 420 ATGACAGCTGTTGATTATATGATGCTCCAGAGTGTGATGATTTTCATTCATCC 479
QY 1427 AGGGCTTGATGTCAAGATTATACCAAGAGTCTTCTACAGAGGCGCAAGAACAA 1486
DB 480 AGGGCTTGATGTCAAGATTATACCAAGAGTCTTCTACAGAGGCGCAAGAACAA 539
QY 1487 ACAGACAGACAGTCCAGACAGACAGATGACCTGACAAAAATGATTTATATGGC 1546
DB 540 ACAGACAGACAGTCCAGACAGACAGATGACCTGACAAAAATGATTTATATGGC 599
QY 1547 TCTATAACTATGTGCCAGACACTATGTGACTTACATAATTTGTCAGAGCTGTCT 1606
DB 600 TCTATAACTATGTGCCAGACACTATGTGACTTACATAATTTGTCAGAGCTGTCT 659
QY 1607 TGCCCTCATGAATTTGGCTCCAAATGAATGAATCTTTCATGACAGTGTAGAGGCC 1666
DB 660 TGCCCTCATGAATTTGGCTCCAAATGAATGAATCTTTCATGACAGTGTAGAGGCC 719
QY 1667 TGACCAAGATTTCCCAAGAGG 1687
DB 720 TGACCAAGATTTCCCAAGAGG 740

RESULT 31
AI968397/c 527 bp mRNA linear EST 09-MAR-2000
LOCUS wu02f07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2515813 3,
DEFINITION mRNA sequence.
ACCESSION AI968397
VERSION AI968397.1 GI:5765215
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
1 (bases 1 to 527)
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1050 Std Error: 0.00
Seq primer: -40up from Gibco
High quality sequence stop: 449.
Location/Qualifiers
1. 527
/organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2515813"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_id="NCI_CGAP GC6"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI_CGAP GC4 was prepared, and
as circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."

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ORIGIN

```

Query Match      15.3%; Score 414; DB 1; Length 527;
Best Local Similarity 99.6%; Pred. No. 3.3e-169;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 802 GACAGAGAGAGTACATTGAAAGAGAGAGAGTGGACATTTGCGGAAACTCTTACA 861
DB 527 GACAGAGAGAGTACATTGAAAGAGAGAGAGTGGACATTTGCGGAAACTCTTACA 468
QY 862 TATGCCCCCATTTGAGAGAGACAGAGTACGACACAAATCCCTACATTAAGAACAA 921
DB 467 TATGCCCCCATTTGAGAGAGACAGAGTACGACACAAATCCCTACATTAAGAACAA 408
QY 922 TCCTAAGAGAGATCCAGCAATACGCTTACTCTGAGTGAATACCGAAAAAGATGG 981
DB 407 TCCTAAGAGAGATCCAGCAATACGCTTACTCTGAGTGAATACCGAAAAAGATGG 348
QY 982 AAAATCCCATCTACTGCTCAAGATGCCAGACACCAAGGCTATTTGCTATGAGATG 1041
DB 347 AAAATCCCATCTACTGCTCAAGATGCCAGACACCAAGGCTATTTGCTATGAGATG 288
QY 1042 TTAATCTAGACAGAGTCCATCCCTTAAGTCTGCTCAAAAAAACAATCTCGGCC 1101
DB 287 TTAATCTAGACAGAGTCCATCCCTTAAGTCTGCTCAAAAAAACAATCTCGGCC 228
QY 1102 CAAGAAGAAATCAGAGAAATTCATCTGATTTGACTAGAAACATCAAGAGATGAGA 1161
DB 227 CAAGAAGAAATCAGAGAAATTCATCTGATTTGACTAGAAACATCAAGAGATGAGA 168
QY 1162 ACCTGACTTTTTCAGAGTAAATTAATCTGATGCTTTTGAATTTAAGATTGCTA 1221
DB 167 ACCTGACTTTTTCAGAGTAAATTAATCTGATGCTTTTGAATTTAAGATTGCTA 108
QY 1222 ATTCCATCCACTGCTGGAATCTCCCTCAAAAGGTTTAAATCACTTCAATCCCAA 1281
DB 107 ATTCCATCCACTGCTGGAATCTCCCTCAAAAGGTTTAAATCACTTCAATCCCAA 48
QY 1282 AATGGAGTTGTGATGTCAAGAAACCATATAAAAAAG 1317
DB 47 AATGGAGTTGTGATGTCAAGAAACCATATAAAAAAG 12

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RESULT 32
BE467670/c 457 bp mRNA linear EST 27-JUL-2000
LOCUS h267607.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213061 3',
DEFINITION mRNA sequence.
ACCESSION BE467670
VERSION BE467670.1 GI:9513445
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 457)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

```

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JOURNAL
COMMENT
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL, send email to:
linfimage.linl.gov
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..457

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FEATURES
source
1..457

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3213061"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_id="NCI_CGAP_Lu24"
/notes="Organ: Lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Lu5 was prepared, and as circles were
used in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (cloneids
141920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."

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ORIGIN

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Query Match      15.0%; Score 406; DB 2; Length 457;
Best Local Similarity 99.8%; Pred. No. 1e-165;
Matches 456; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 854 TCCTACATATATGCCCCCATTTCTGAGAGAAACAGAGTACGACACAAATCCCTCACTTA 913
DB 457 TCCTACATATATGCCCCCATTTCTGAGAGAAACAGAGTACGACACAAATCCCTCACTTA 398
QY 914 TAGAACAATCTTAAAGAGATCCAGCAATACGCTTACTCCAGTGTGAATATACGAA 973
DB 397 TAGAACAATCTTAAAGAGATCCAGCAATACGCTTACTCCAGTGTGAATATACGAA 338
QY 974 AAAGATGAAAAATCCCACTCACTGCTCAAGATGCCAGACACCAAGGCTATTGCTTA 1033
DB 337 AAAGATGAAAAATCCCACTCACTGCTCAAGATGCCAGACACCAAGGCTATTGCTTA 278
QY 1034 TGGAAATGTTTATTAAGACAGAGTCACTCCCTTAAGTCTGCTCAAAAAAACAAT 1093
DB 277 TGGAAATGTTTATTAAGACAGAGTCACTCCCTTAAGTCTGCTCAAAAAAACAAT 218
QY 1094 TCTCGGCCCAAGAAACATCAGAGAAATTCATCTGATGCTTTGATAGAAACATCAAGAG 1153
DB 217 TCTCGGCCCAAGAAACATCAGAGAAATTCATCTGATGCTTTGATAGAAACATCAAGAG 158
QY 1154 AATGAAGAAAGTGAATTTTTCAGAGTAAATTAATCTGATGCTTTTGAATTTAAG 1213
DB 157 AATGAAGAAAGTGAATTTTTCAGAGTAAATTAATCTGATGCTTTTGAATTTAAG 98
QY 1214 AGTTGTAATTCATCACTGCTGAGAAATTCCTCAAAAGGTTTATCACTTC 1273
DB 97 AGTTGTAATTCATCACTGCTGAGAAATTCCTCAAAAGGTTTATCACTTC 38
QY 1274 ATCCCAAAAATGGAGTTGTGAATGTCAAGAAACCATTA 1310
DB 37 ATCCCAAAAATGGAGTTGTGAATGTCAAGAAACCATTA 1

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RESULT 33
AM026300/c 657 bp mRNA linear EST 09-MAR-2000
LOCUS AM026300

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DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
FEATURES	
Db	Query Match Best Local Similarity 99.8%; Pred. No. 1.le-162; Matches 449; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	14.8%; Score 399; DB 2; Length 657;
Db	630 GCCAGAAACCCTGTCAGCAAAAATTCTGCAGGCCCATCCTTGCGAGAGACTTGTGA 689
OY	450 GCCAGAACCCCTGTACAGCAAACTTCTCAAGCCCCATCCTTGCGAGAGACTTGTGA 391
Db	690 GGATGCTGTATNAGCCCAAGTTCCGTCATGGGCTCCGTTGCTCTGTTGGTGGCCCTC 749
OY	390 GGATGCTGTATNAGCCCAAGTTCCGTCATGGGCTCCGTTGCTCTGTTGGTGGCCCTC 331
Db	750 CTGCTCACTCTCTTTGTACTGGGGCTAATTTCTTTGTGTTTCTGAAGAAGACAAGAA 809
OY	330 CTGCTCACTCTCTTTGTACTGGGGCTAATTTCTTTGGTCTCTGAAGAAGACAAGAA 271
Db	810 GAGTACATTGAAGAAGAGAAGAGTGAACATTTGTGGGAACTCCTTAACATATGCCCC 869
OY	270 GAGTACATTGAAGAAGAGAAGAGTGAACATTTGTGGGAACTCCTTAACATATGCCCC 211
Db	870 CATTCGTGAAGAACAACAAGATAGACACATCCCTCACACATAATAGAAACATCCTTAA 929
OY	210 CATTCGTGAAGAACAACAAGATAGACACATCCCTCACACATAATAGAAACATCCTTAA 151

QY	930	GAAGATCCAGAAATATACGTTTACTCCACGTGTGAAATACCGAAAGATGGAATATCCC	968
DB	150	GAAGATCCAGAAATATACGTTTACTCCACGTGTGAAATACCGAAAGATGGAATATCCC	91
QY	990	CATCCTACTGCTCAGATGCCAGACACACCAAGGCTATTGGCTATGGAATGTTATCTAG	1049
DB	90	CATCCTACTGCTCAGATGCCAGACACACCAAGGCTATTGGCTATGGAATGTTATCTAG	31
QY	1050	ACAGCAGTGCACCTCCCTAAGTCTCTGCTC	1079
DB	30	ACAGCAGTGCACCTCCCTAAGTCTCTGCTC	1
RESULT 34			
LOCUS	BO898498	968 bp	mRNA
DEFINITION	AGENCOURT 8228971 Lupski dorsal root ganglion Homo sapiens cDNA		EST 16-AUG-2002
ACCESSION	BO898498		
VERSION	BO898498.1	GI:22290512	
KEYWORDS	EST.		
ORGANISM	Homo sapiens (human)		
SOURCE	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
TITLE	1 (bases 1 to 968)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cga@rs-remail.nih.gov		
	Tissue Procurement: Dr. James R. Lupski		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		
	Plate: L1AM13567 row: 1 column: 16		
	High quality sequence, stop: 611.		
FEATURES	Location/Qualifiers		
source	1..968		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon.9606"		
	/clone="IMAGE:6182103"		
	/sex="male"		
	/tissue_type="dorsal root ganglia"		
	/dev_stage="adult, 36 yr"		
	/lab_host="DH10B"		
	/clone_lib="Lupski dorsal root ganglion"		
	/note="vector: pCMV-Sport6 (Life Technologies); Site_1:		
	NotI; Site_2: SalI; cDNA made by oligo-dT priming.		
	Directionally cloned using the following adaptors:		
	5'-TCGACCAACGCGTCG-3' and		
	5'-GACTAGTCTGATGCGAGCGCGCCCT(15)-3'. Size selected >		
	1 kb for average insert length 1.7 kb. This is a primary		
	library, non-amplified. Library constructed by Life		
	Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor		
	College of Medicine) and is available through Life		
	Technologies."		
ORIGIN			
Query Match	14.7%	Score 398;	DB 5; Length 968;
Best Local Similarity	99.6%	Pred. No. 2,96-162;	
Matches	568; Conservative	0; Mismatches	1; Indels
			1; Gaps
QY	915	AGAACATCCCTAAAGAGAAATCCAGCAATACGTTTACTCTCACTGTGAAATACCGAAA	974
DB	194	AGAACATCCCTAAAGAGAAATCCAGCAATACGTTTACTCTCACTGTGAAATACCGAAA	253
QY	975	AAGATGAGAAATCCCACTCACTGCTCAAGATGCAGATGCACACACCAAGGCTATTGGCTAT	1034

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Db      254 AAGTGGAAATATCCCACTCACTGCTCAAGATGCGACACACCAAGCTATTGGCTAT 313
Qy      1035 GAGATATTATCTAGACAGACAGTCACTCCCTTAAGTCTGCTC-AAAAAAAAACAAT 1093
Db      314 GAGATATTATCTAGACAGACAGTCACTCCCTTAAGTCTGCTCAAAAAAAAAACAAT 373
Qy      1094 TCTCGGCCCAAGAAACATCAAGAAATTCATGATTTGACAGAAACATCAAGAG 1153
Db      374 TCTCGGCCCAAGAAACATCAAGAAATTCATGATTTGACAGAAACATCAAGAG 433
Qy      1154 AATGAAGAGCTGACCTTTTTCAGAGATTAATATCTGATGCTTTAGATTAA 1213
Db      434 AATGAAGAGCTGACCTTTTTCAGAGATTAATATCTGATGCTTTAGATTAA 493
Qy      1214 AGTTCTGAATTCATCACTGCTGAGAAATCTCTCAACCCAGAGGTTTATCACTTC 1273
Db      494 AGTTCTGAATTCATCACTGCTGAGAAATCTCTCAACCCAGAGGTTTATCACTTC 553
Qy      1274 ATCCCAAAATGGAGATTGTGAATGTCAAGCAACATAAAAAGTGTGAAATATTC 1333
Db      554 ATCCCAAAATGGAGATTGTGAATGTCAAGCAACATAAAAAGTGTGAAATATTC 613
Qy      1334 TATAGAAATGTAATGCAAGCTCAACATATTAATGACAGCTGTTGATTAATGATGC 1393
Db      614 TATAGAAATGTAATGCAAGCTCAACATATTAATGACAGCTGTTGATTAATGATGC 673
Qy      1394 TCCAGGTCACTGCTGAGTTTCATTCATCCAGGCTTGATGATGAGATTAATCA 1453
Db      674 TCCAGGTCACTGCTGAGTTTCATTCATCCAGGCTTGATGATGAGATTAATCA 733
Qy      1454 GAGCTTGTACAGAGGCGCAAGAAC 1483
Db      734 GAGCTTGTACAGAGGCGCAAGAAC 763

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RESULT 35
BU617383/c 663 bp mRNA linear EST 23-SEP-2002
LOCUS DEFINITION
UI-H-DF0-bew-1-13-0-UI.s1 NCI_CGAP_DF0 Homo sapiens cDNA clone
BU617383
UI-H-DF0-bew-1-13-0-UI 3', mRNA sequence.
ACCESSION
BU617383.1 GI:23283598
VERSION
EST.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 70-115, >MER1A/UTR/MER4-group (matched complement)
374-650, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

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FEATURES
source
location/Qualifiers
1..663
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-DF0-bew-1-13-0-UI"
/tissue_type="Subchondral Bone"

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/dev stage="Adult"
/lab host="DH10B (Life Technologies)"
/clone lib="NCI_CGAP_DF0"
/note="Organ: Bone; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site: 1: Ecor I; Site 2: Not I;
NCI CGAP DF0 is a cDNA library containing the following
tissue(s): Subchondral Bone. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an Ecor I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GTTAAAGGCTC.
TAG_TISSUE=subchondral bone
TAG_LIB=UI-H-DF0
TAG_SEQ=GTAAAGGCTC"

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ORIGIN
Query Match 14.7%; Score 397; DB 5; Length 663;
Best Local Similarity 99.8%; Pred. No. 8.4e-162;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      2255 GAGGTGCGAGTGAAGTGAAGTGCACCACTCCGGCTTGGCAAGGCAAAAC 2314
Db      448 GAGGTGCGAGTGAAGTGAAGTGCACCACTCCGGCTTGGCAAGGCAAAAC 389
Qy      2315 TCCAAATACAAACAAACAAACACCTGTGCTAGGTCACTGCAAGTGAATGACA 2374
Db      388 TCCAAATACAAACAAACAAACACCTGTGCTAGGTCACTGCAAGTGAATGACA 329
Qy      2375 TCCCTACCAACACAGAGCTCACCATCTTTATCTTAAGTGAAGAAACATGGGAGGGA 2434
Db      328 TCCCTACCAACACAGAGCTCACCATCTTTATCTTAAGTGAAGAAACATGGGAGGGA 269
Qy      2435 AAGGGGAATGGCGCTTTTGATATGTTCCCTGAGCATATCTTGAATGGAGCTCCCTTA 2494
Db      268 AAGGGGAATGGCGCTTTTGATATGTTCCCTGAGCATATCTTGAATGGAGCTCCCTTA 209
Qy      2495 CCAAGTGAATGAAGTGTGAAACCTTAATACAAATGCTTGTGGGCAAGATGGGATT 2554
Db      208 CCAAGTGAATGAAGTGTGAAACCTTAATACAAATGCTTGTGGGCAAGATGGGATT 149
Qy      2555 GAGGATTAATCTTCTCTCAAGAAAGCAATGTAAGGAATTGAGCCAGATCTCTCCCTAC 2614
Db      148 GAGGATTAATCTTCTCTCAAGAAAGCAATGTAAGGAATTGAGCCAGATCTCTCCCTAC 89
Qy      2615 TGCMAAACCTTATGTAAGTAAGTAAGTCTTTACTATCTTAATTAACAGATATTGG 2674
Db      88 TGCMAAACCTTATGTAAGTAAGTAAGTCTTTACTATCTTAATTAACAGATATTGG 29
Qy      2675 AGATTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2702
Db      28 AGATTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1

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RESULT 36
BQ000581 705 bp mRNA linear EST 17-JUN-2002
LOCUS DEFINITION
UI-H-DPO-avv-d-09-0-UI.s1 NCI_CGAP_F01 Homo sapiens cDNA clone
BQ000581
IMAGE:584376 3', mRNA sequence.
ACCESSION
BQ000581
VERSION
BQ000581.1 GI:19725481
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE

```


JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mary Hendrix
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNI at: <http://image.llnl.gov>
The following repetitive elements were found in this cDNA
sequence: 70-115, >MER31A#LTR/MER4-group (matched complement)
374-663, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..705
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5884376"
/issue_type="Fibrosarcoma"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_Fs1"
/note="Vector: pT73-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP_Fs1 is
a cDNA library containing the following tissue(s):
Fibrosarcoma Cell line HT-1088 (ATCC number CCL-121). The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT73-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GTTCTACGAG.
TAG_TISSUE=fibrosarcoma
TAG_LIB=UI-H-DPO
TAG_SEQ=GTCTACGAG"

ORIGIN

Query Match 14.1%; Score 380; DB 5; Length 705;
Best Local Similarity 99.8%; Pred. No. 2.2e-154;
Matches 430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2255 GAGGTTGCGATGAGTGCATGCGACCTCCGCTTAGGCAAGAGCAAAAC 2314
DB 448 GAGGTTGCGATGAGTGCATGCGACCTCCGCTTAGGCAAGAGCAAAAC 389
QY 2315 TCCATATCAAAACAAACAAACACCTGTGCTAGGTCAGTCCGACGTAAGATGAGA 2374
DB 388 TCCATATCAAAACAAACAAACACCTGTGCTAGGTCAGTCCGACGTAAGATGAGA 329
QY 2375 TCCCTACCAACACAGAGCTCACCATCTTTATACCTTAAGTGAACAAATGCGGAAGCGGA 2434
DB 328 TCCCTACCAACACAGAGCTCACCATCTTTATACCTTAAGTGAACAAATGCGGAAGCGGA 269
QY 2435 AAGGGGAATGCGCTTTTGATATGTTCCCTGACGATATCTTGAATGAGACCTCCCTA 2494
DB 268 AAGGGGAATGCGCTTTTGATATGTTCCCTGACGATATCTTGAATGAGACCTCCCTA 209
QY 2495 CCAAGGATGAAGTGTGAAAAAATTATTAACAATGCTGTGGGCAAGATGGGATT 2554
DB 208 CCAAGGATGAAGTGTGAAAAAATTATTAACAATGCTGTGGGCAAGATGGGATT 149
QY 2555 GAGGATATCTTCTCTCAGAAAGGATGTGAAGAAATGAGCCAGATCTCTCCCTAC 2614
DB 148 GAGGATATCTTCTCTCAGAAAGGATGTGAAGAAATGAGCCAGATCTCTCCCTAC 89
QY 2615 TCGAAAAACCTATGTAGTAAAAAGTCTTCTTACTTATTTAAACAGATATTGG 2674

DB 88 TCGAAAAACCTATGTAGTAAAAAGTCTTCTTACTTATTTAAACAGATATTGG 29
QY 2675 AGATTACATA 2685
DB 28 AGATTACATA 18

RESULT 37
CD366710/c
LOCUS
DEFINITION
UI-H-FT2-bjo-n-03-0-UI s1 NCI CGAP_Ft2 Homo sapiens cDNA clone
ACCESSION
CD366710
VERSION
CD366710.1 GI:31150800
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
sequence: 70-115, >MER31A#LTR/MER4-group (matched complement)
374-663, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..712
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjo-n-03-0-UI"
/issue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_Ft2"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP_Ft2 is a subtracted cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph
aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
The library was subtracted according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. The tissue
was provided by Dr. Gary W. Hunninghake of the University
of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2

ORIGIN

TAG_SEQ=GGCCATGCCG"

Db	61	AAAAACCCATTTGTATATAAAAAAGCTTCTTTACTATCTTAATTAACAAGATTGTGA	4
RESULT 41			
LOCUS	CD630759	761 bp	mRNA linear EST 12-JAN-2004
DEFINITION	56071680J1 FLP Homo sapiens cDNA, mRNA sequence.		
ACCESSION	CD630759		
VERSION	CD630759.1	GI:40279025	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 761)		
TITLE	Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.		
JOURNAL	Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes		
COMMENT	Genomics 84 (1), 205-210 (2004)		
CONTACT	Incyte Genomics, Inc.		
3160 Porter Dr., Palo Alto, CA 94304, USA			
Tel: 6508454102			
Email: gfu@incyte.com.			
FEATURES	Location/Qualifiers		
Source	1..761		
/organism="Homo sapiens"			
/mol_type="mRNA"			
/db_xref="taxon:9606"			
/clone_lib="FLP"			
/note="Vector: pDrive Cloning Vector"			
ORIGIN			
Query Match	13.6%; Score 367; DB 6; Length 761;		
Best Local Similarity	100.0%; Pred. No. 1e-148;		
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	763 TTGTACTGGGGCTATTCTTTGTTCTTGAAGAGAGAGACAAGAAAGTACATTGAAG	822	
DB	35 TTGTACTGGGGCTATTCTTTGTTCTTGAAGAGAGAGACAAGAAAGTACATTGAAG	94	
QY	823 AGAAGAAAGAGTGGACATTTGTGGGAAATCTCTTAACATATGCCCCATTCTGGAGAGA	882	
DB	95 AGAAGAAAGAGTGGACATTTGTGGGAAATCTCTTAACATATGCCCCATTCTGGAGAGA	154	
QY	883 ACACAGAGTACGACACAAATCCCTCACACTAATATAGAACAACTCTAAGGAAGATCCAGCA	942	
DB	155 ACACAGAGTACGACACAAATCCCTCACACTAATATAGAACAACTCTAAGGAAGATCCAGCA	214	
QY	943 ATACGCTTACTCCACTGTGTGAAATACCGAAGAAAGATGGAATATCCCACTCATGTGCTA	1002	
DB	215 ATACGCTTACTCCACTGTGTGAAATACCGAAGAAAGATGGAATATCCCACTCATGTGCTA	274	
QY	1003 CGATGCCAGACACACAAAGGCTATTGTGCTATGAGATGTTATCTAGACAGCAGTGCACT	1062	
DB	275 CGATGCCAGACACACAAAGGCTATTGTGCTATGAGATGTTATCTAGACAGCAGTGCACT	334	
QY	1063 CCCCTAAGTCTCTGCTCAAAAAAACAATTCGCGGCCAAAGAAAAACAATCAGAGAA	1122	
DB	335 CCCCTAAGTCTCTGCTCAAAAAAACAATTCGCGGCCAAAGAAAAACAATCAGAGAA	394	
QY	1123 TTCACTG 1129		
DB	395 TTCACTG 401		
RESULT 42			
LOCUS	CD630761	793 bp	mRNA linear EST 12-JAN-2004
DEFINITION	56071688J1 FLP Homo sapiens cDNA, mRNA sequence.		
ACCESSION	CD630761		
VERSION	CD630761.1	GI:40279027	

KEYWORDS	EST
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euleleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS	1 (bases 1 to 793)
TITLE	Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
JOURNAL	Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
COMMENT	Genomics 84 (1), 205-210 (2004)
CONTACT	Contact: Fu GK
INCYTE	Incyte Genomics, Inc.
PORTER	3160 Porter Dr., Palo Alto, CA 94304, USA
TEL	Tel: 6508454102
EMAIL	Email: gfu@incyte.com.
LOCATION	location/Qualifiers
FEATURES	1..793
SOURCE	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone_id="FLP"
	/note="Vector: pDrive Cloning Vector"
ORIGIN	
Query Match	13.3%; Score 360; DB 6; Length 793;
Best Local Similarity	99.2%; Pred. No. 1.1e-145;
Matches 730; Conservative	0; Mismatches 5; Indels 1; Gaps 1;
QY	782 TTGGTTCTGAAGAGAGAGAGAGAGAGTACATTTAGAGAGAGAGAGAGTGCAT 841
DB	50 TTGGTTCTGAAGAGAGAGAGAGAGAGTACATTTAGAGAGAGAGAGAGTGCAT 109
QY	842 TTGTGGGAACTCTTAACATATGCCCCATTTGAGAGACACAGATGACACAAAT 901
DB	110 TTGTGGGAACTCTTAACATATGCCCCATTTGAGAGACACAGATGACACAAAT 169
QY	902 CCTCACACTAATGAACAATCTTAAGAAGATCCAGCAATACGGTTTACTTCACTGT 961
DB	170 CCTCACACTAATGAACAATCTTAAGAAGATCCAGCAATACGGTTTACTTCACTGT 229
QY	962 GGAATCCGAAAGATGGAAGATCCCACTACGCTCAGATGCCAGACACCAAG 1021
DB	230 GGAATCCGAAAGATGGAAGATCCCACTACGCTCAGATGCCAGACACCAAG 289
QY	1022 GCTATTTGCTATGAGATGTTATCTGAGACAGAGTGCATCCCTTAAGTCTGTGCTCA 1081
DB	290 GCTATTTGCTATGAGATGTTATCTGAGACAGAGTGCATCCCTTAAGTCTGTGCTC-A 348
QY	1082 AAAAAAACAATCTCGGCCCAAGAAACAATCAGAGAATTCAGTATTGACTAGAA 1141
DB	349 AAAAAAACAATCTCGGCCCAAGAAACAATCAGAGAATTCAGTATTGACTAGAA 408
QY	1142 ACATCAGAGAAATGAAGAACTTGACTTTTTCCAGATTAATATCTCTGATGCTTC 1201
DB	409 ACATCAGAGAAATGAAGAACTTGACTTTTTCCAGATTAATATCTCTGATGCTTC 468
QY	1202 TTAGATTTAAGAGTTGCTATTTCCATCCACTGCTGAGAAATCTCCCAACCAGAGG 1261
DB	469 TTAGATTTAAGAGTTGCTATTTCCATCCACTGCTGAGAAATCTCCCAACCAGAGG 528
QY	1262 TTATATCACTTCATCCCAAAATGGGATTTGTGAATGTCAGCAAAACCAATAAAAAAGTGCT 1321
DB	529 TTATATCACTTCATCCCAAAATGGGATTTGTGAATGTCAGCAAAACCAATAAAAAAGTGCT 588
QY	1322 TAGAAGTATTCCTATGAAATGTAAATGCAAGTCAACATATTAATGACAGCTGTGT 1381
DB	589 TAGAAGTATTCCTATGAAATGTAAATGCAAGTCAACATATTAATGACAGCTGTGT 648
QY	1382 ATTAAATGATGGCTCCAGGTCAAGTGTGCGAGTTTCAATCCAGGGCTTGATGTCA 1441
DB	649 ATTAAATGATGGCTCCAGGTCAAGTGTGCGAGTTTCAATCCAGGGCTTGATGTCA 708
QY	1442 GATATTACCAAGATCTGCTTCCAGAGGGCCAGAGACCAAAACAGACAGCAAGTC 1501

|||||
Db 709 GGATTATACCAAGAGCTTGCTACAGAGGCGCAAGAACCAAAACAGACAGACAAGTC 768
1502 CAGCAGACAGATGC 1517
|||||
Db 769 CAGCAGAGCAGATGC 784
|||||

RESULT 43
BE246373
LOCUS BE246373
DEFINITION BE246373 442 bp mRNA linear EST 03-OCT-2001
TCBAP1E908 pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2908, mRNA
sequence.
ACCESSION BE246373
VERSION BE246373.1 GI:9098122
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 442)
Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R.,
Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
Pediatric Leukemia cDNA Sequencing Project
Unpublished (2000)
CONTACT: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, WC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@xccc.org
Citation: Carinci,P. and Hayashizaki,Y. High efficiency
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Seq primer: M13 primer.
Location/Qualifiers
1. 442
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TCBAP2908"
/sex="male"
/cissue_type="Leukopheresis"
/cell_type="Pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/clone_lib="Pediatric pre-B cell acute lymphoblastic
leukemia Baylor-HGSC project=TCBA"
/note="Vector: lambda pSB, Site 1: BamHI, Site 2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'-GGAGACTCGACGGCCGCGCAGAGAG(T)VN
3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand
was primed with a BamHI-dC primer
[5'-AGAGACTCGATCCGCGCCGCCCAATATATAT(C) 3'].
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of
lambda pSB vector. Library went through one round of
normalization. Library was constructed by Wei Yu at RIKEN
of Japan (Carinci P, Westover A, Nishiyama Y, Ohsuni T,
Itoh M, Nagaoka S, Sasaki, Okazaki Y, Muramatsu M,
Schneider C, Hayashizaki Y, High efficiency selection of
full-length cDNA by improved bicinylated cap trapper.,
DNA Res 4: 1, 61-6, Feb 28, 1997)"

ORIGIN
Query Match 13.2%; Score 358; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 9,1e-145;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 AGCAGCTGTCAAGAGCTTAAGTACCATGGGTCTGCAGAGCAATTAAGATGGCAGCTGTG 477
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DB 85 AGCAGCTGTCAAGAGCTTAAGTACCATGGGTCTGCAGAGCAATTAAGATGGCAGCTGTG 144
|||||

QY 478 TGACCAATCTGACATGCTGACATGGAACATGGGGAAGAGATGTGATTTATACCTGGAGG 537
|||||
DB 145 TGACCAATCTGACATGCTGACATGGAACATGGGGAAGAGATGTGATTTATACCTGGAGG 204
|||||

QY 538 CCTTGCGGCGACAGCAGCCAAATGATGTCCTCATATGGTCCATCTCTCCCATCTCTGGAGAT 597
|||||
DB 205 CCTTGCGGCGACAGCAGCCAAATGATGTCCTCATATGGTCCATCTCTCCCATCTCTGGAGAT 264
|||||

QY 598 GGGGGAAGAAATGATATGACCTTCATCTGCTGCGCAGGAACCTTCGACAGAACTTCT 657
|||||
DB 265 GGGGGAAGAAATGATATGACCTTCATCTGCTGCGCAGGAACCTTCGACAGAACTTCT 324
|||||

QY 658 CAAGCCCATCTCTGCGCAGGAAGCTCTGGAAGTCTGCTGATGACCCAGATTCCTCCA 717
|||||
DB 325 CAAGCCCATCTCTGCGCAGGAAGCTCTGGAAGTCTGCTGATGACCCAGATTCCTCCA 384
|||||

QY 718 TGGTCTCTCTGTGCTCTCTGTTGGTCCCTCTGCTCAGTCTCTTTGACTGGGACT 775
|||||
DB 385 TGGTCTCTCTGTGCTCTCTGTTGGTCCCTCTGCTCAGTCTCTTTGACTGGGACT 442
|||||

RESULT 44
AM197989
LOCUS AM197989/C 354 bp mRNA linear EST 29-NOV-1999
DEFINITION AM197989
RNA sequence.
ACCESSION AM197989.1 GI:6477219
VERSION AM197989
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 354)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/hrp/image/image.html
Seq primer: 40UP from Gibco.
Location/Qualifiers
1. 354
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2705352"
/cissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Panel"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN
Query Match 13.1%; Score 354; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 5,2e-143;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1685 GGGCCAGGTGTGATCCACAGGACTTGAAGTCAAGTTCAAAAGATGAAGATCAAGG 1744
|||||
DB 354 GGGCCAGGTGTGATCCACAGGACTTGAAGTCAAGTTCAAAAGATGAAGATCAAGG 295
|||||

QY 1745 TAGCTGACCATGTTTGGCAATATATATGAGACACAGAAAGTGTGATGCCCCAAGA 1804
|||||
DB 294 TAGCTGACCATGTTTGGCAATATATATGAGACACAGAAAGTGTGATGCCCCAAGA 235
|||||

QY 1805 CAAGACCTCCAGCAGGCTTCATTATGACCTGTGTGCTGCAAAAGAAAGTCTAGTTT 1864
 DB 234 CAAGACCTCCAGCAGGCTTCATTATGACCTGTGTGCTGCAAAAGAAAGTCTAGTTT 175
 QY 1865 TAAGCTGTGCGAAGCCATCCCAATTAAGAGACCGAGTCTGAAGTCACTTTAAATC 1924
 DB 174 TAAGCTGTGCGAAGCCATCCCAATTAAGAGACCGAGTCTGAAGTCACTTTAAATC 115
 QY 1925 TAGGTGTGAGACTTGTGAGTCAAGCAGTGTGTGTGGGCGACGGGGGCGAGTGGTAC 1984
 DB 114 TAGGTGTGAGACTTGTGAGTCAAGCAGTGTGTGTGGGCGACGGGGGCGAGTGGTAC 55
 QY 1985 TTGTAACTTTAAAGATGTTAATTCATTCAATAGATATTTATTAAGAACTTA 2038
 DB 54 TTGTAACTTTAAAGATGTTAATTCATTCAATAGATATTTATTAAGAACTTA 1
 RESULT 45
 AI989857/c 405 bp mRNA linear EST 08-MAR-2000
 LOCUS w36c08.x1 NCI_CGAP_G66 Homo sapiens cDNA clone IMAGE:249278 3'
 DEFINITION similar to contains Alu repetitive element; mRNA sequence.
 ACCESSION AI989857 GI:5836738
 VERSION AI989857.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 405)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.llnl.gov/bdrp/image/image.html
 Insert Length: 473 Std Error: 0.00
 Seq primer: -40UP from Gibco.
 Location/Qualifiers
 FEATURES
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 1. 405
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:249278"
 /issue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_G66"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
 from the normalized library NCI CGAP G64 was prepared, and
 88 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (cloneids
 1257096-1258631, 1469064-1470983, and 1475592-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaldo. "
 ORIGIN
 Query Match 13.1%; Score 354; DB 1; Length 405;
 Best Local Similarity 99.8%; Pred. No. 5,Je-113;
 Matches 404; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2288 CTCGGGCTAGGCAAGAGCAAACTCCAAATACAAACAAACAAACACTGTGCT 2347

DB 405 CTCGGGCTAGGCAAGAGCAAACTCCAAATACAAACAAACAAACACTGTGCT 346
 QY 2348 AGGTCACTCTGCGACGTAAGATGACATCTCTTCAACACAGAGCTCACCATTCTTATA 2407
 DB 345 AGGTCACTCTGCGACGTAAGATGACATCTCTTCAACACAGAGCTCACCATTCTTATA 286
 QY 2408 CTTAAGTGAAGAAACATGGGGAAGGGGAAAGGGGATGGCTTTGATATGTTCCCTGA 2467
 DB 285 CTTAAGTGAAGAAACATGGGGAAGGGGAAAGGGGATGGCTTTGATATGTTCCCTGA 226
 QY 2468 CGCATATCTTGAATGAGACCTCTCCACCAAGTATGAAAGTGTGAAAACTTAATTAAC 2527
 DB 225 CACATATCTTGAATGAGACCTCTCCACCAAGTATGAAAGTGTGAAAACTTAATTAAC 166
 QY 2528 AAATGCTGTGGGCAAGAAATGGATTTGAGATTATCTTCTCAGAAAGCAATTGTGAA 2587
 DB 165 AAATGCTGTGGGCAAGAAATGGATTTGAGATTATCTTCTCAGAAAGCAATTGTGAA 106
 QY 2588 GGAATTGAGCCAGATCTCTCCCTACTGCAAAACCTATTGTAGTAAAGATCTTCTT 2647
 DB 105 GGAATTGAGCCAGATCTCTCCCTACTGCAAAACCTATTGTAGTAAAGATCTTCTT 46
 QY 2648 TACTATCTTAATTAACAGATATTGTGAGATTTCATTAATAAAAAA 2692
 DB 45 TACTATCTTAATTAACAGATATTGTGAGATTTCATTAATAAAAAA 1
 RESULT 46
 AA908670/c 396 bp mRNA linear EST 09-JUN-1998
 LOCUS 0104d01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522465 3'
 DEFINITION similar to contains element L1 repetitive element; mRNA sequence.
 ACCESSION AA908670 GI:3048075
 VERSION AA908670.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 396)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.llnl.gov/bdrp/image/image.html
 Insert Length: 781 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 360.
 Location/Qualifiers
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 1. 396
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1522465"
 /issue_type="carcinoid"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Lu5"
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; 1st strand cDNA was prepared from a
 neuroendocrine lung carcinoid, and was then primed with a
 Not I - oligo(dt) primer. Double-stranded cDNA was ligated
 to Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified

pt773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 12.6%; Score 340; DB 1; Length 396;
Best Local Similarity 99.7%; Pred. No. 6.6e-137;
Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2295 CTAGGCAACGAGCAAACTCCATATACAAACAAACAAACCTGTGCTAGCTGAG 2354
DB 396 CTAGGCAACGAGCAAACTCCATATACAAACAAACAAACCTGTGCTAGCTGAG 337
QY 2355 TCTGGACACGTAGATGAAATCCCTCAACACAGAGCTCACCATCTTTATATCTTAAT 2414
DB 336 TCTGGACACGTAGATGAAATCCCTCAACACAGAGCTCACCATCTTTATATCTTAAT 277
QY 2415 GAAAAACATGGGGAAGGGGAATGGCTTTTGTATGTTCCTTGCATCGATAT 2474
DB 276 GAAAAACATGGGGAAGGGGAATGGCTTTTGTATGTTCCTTGCATCGATAT 217
QY 2475 CTTGAATGAGACCTCCCTACCAAGTATGAAAGTTGTTGAAAACTTAATACAAATGCT 2534
DB 216 CTTGAATGAGACCTCCCTACCAAGTATGAAAGTTGTTGAAAACTTAATACAAATGCT 157
QY 2535 TGTGGGCAAGAAATGGGATTTAGATTTATCTTCTCAGAAAGCATTTGTGAAGATTG 2594
DB 156 TGTGGGCAAGAAATGGGATTTAGATTTATCTTCTCAGAAAGCATTTGTGAAGATTG 97
QY 2595 AGCGAATCTCTCTCCCTACCTGCAAAACCTATGTATGAAAAAGTCTTTTACTATTC 2654
DB 96 AGCGAATCTCTCTCCCTACCTGCAAAACCTATGTATGAAAAAGTCTTTTACTATTC 37
QY 2655 TTAATTAACAGATATTGTAGATTGACATA 2685
DB 36 TTAATTAACAGATATTGTAGATTGACATA 6

RESULT 47
AM630293 426 bp mRNA linear EST 31-MAR-2000
LOCUS hb81a11.y1 NCI_CGAP_GUI Homo sapiens cDNA clone IMAGE:2969180 5'
DEFINITION similar to TR:014775 Q14775 Lf-9 PRECURSOR; mRNA sequence.
ACCESSION AM630293.1 GI:7377083
VERSION AM630293.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 426)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Other ESTs: hb81a11.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christina Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/resources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 424.
Location/Qualifiers
1..426
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2969180"

FEATURES

source

/tissue_type="2 pooled high-grade transitional cell
tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GUI"
/note="Organ: genitourinary tract; Vector: pCMV-Sport6;
Site_1: Sail; Site_2: NCI; Cloned unidirectionally.
Primer: Oligo dt. Library constructed by Life
Technologies."

ORIGIN

Query Match 12.6%; Score 340; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 6.5e-137;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 417 GAGCACCTGTCAAAAGCTTAAGTACCATGGGTCTGACAGCAATAGATGACCTGT 476
DB 87 GAGCACCTGTCAAAAGCTTAAGTACCATGGGTCTGACAGCAATAGATGACCTGT 146
QY 477 GTGACCAATCTGACATGCTGCATGGAAATGGGAAAGAGATGTGATTATACCTGGAG 536
DB 147 GTGACCAATCTGACATGCTGCATGGAAATGGGAAAGAGATGTGATTATACCTGGAG 206
QY 537 GCCCTGGGCAAGCAAGCCAAATGATCCATATAGGTGCTCATCTCCCATCTCCGGAGA 596
DB 207 GCCCTGGGCAAGCAAGCCAAATGATCCATATAGGTGCTCATCTCCCATCTCCGGAGA 266
QY 597 TGGGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 656
DB 267 TGGGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 326
QY 657 TCAAGCCCCATCTCTTCCAGAAAGCTGTGGAAGTGTCTGTATGATGATGATGATGATGATG 716
DB 327 TCAAGCCCCATCTCTTCCAGAAAGCTGTGGAAGTGTCTGTATGATGATGATGATGATGATG 386
QY 717 ATGTCCTCTCTGTCCTCTCTGTCCTCTCTGTCCTCTCTGTCCTCTCTGTCCTCTCTG 756
DB 387 ATGTCCTCTCTGTCCTCTCTGTCCTCTCTGTCCTCTCTGTCCTCTCTGTCCTCTCTG 426

RESULT 48
A1948861/c 372 bp mRNA linear EST 06-SEP-1999
LOCUS wg37d09.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2473457 3'
DEFINITION mRNA sequence.
ACCESSION A1948861
VERSION A1948861.1 GI:5741171
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 372)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmett-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbtp/image/html
Seq primer: -40UP from Gibco
High quality sequence stop: 311.
Location/Qualifiers
1..372
/organism="Homo sapiens"
/mol_type="mRNA"

FEATURES

source

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 935)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCMP/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM826 row: p column: 20
High quality sequence start: 2
High quality sequence stop: 619.
Location/Qualifiers
1..935
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3954307"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOT7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match 11.6%; Score 314; DB 2; Length 935;
Best Local Similarity 99.7%; Pred. No. 1.3e-125;
Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 GGCTGACTTCAGAGCAATATGCTGTTCCCAACATGCTCAACCTCATTTATTC 80
DB 1 GGCTGACTTCAGAGCAATATGCTGTTCCCAACATGCTCAACCTCATTTATTC 60
QY 81 CTTTGGCAGCTCAGAGCTCAGAGCTCTGAGCCCGTGAAGAGCTGTCGTTCCGTT 140
DB 61 CTTTGGCAGCTCAGAGCTCAGAGCTCTGAGCCCGTGAAGAGCTGTCGTTCCGTT 120
QY 141 GGTGGGGCGTGACTTCCCTGAGTCCAAAGTAAAGCAAGTTGACTTATTTGCTGG 200
DB 121 GGTGGGGCGTGACTTCCCTGAGTCCAAAGTAAAGCAAGTTGACTTATTTGCTGG 180
QY 201 ACCTTCAACAAACCCCTCTTGTACCATACAGCCAGAAAGGGGCACTATCATATGACC 260
DB 181 ACCTTCAACAAACCCCTCTTGTACCATACAGCCAGAAAGGGGCACTATCATATGACC 240
QY 261 CAAAAATCGTAATGGAGAGAGTAAAGCTTCCCAAGATGAGAGCTACCTCCGTAAGCTCAGC 320
DB 241 CAAAAATCGTAATGGAGAGAGTAAAGCTTCCCAAGATGAGAGCTACCTCCGTAAGCTCAGC 300
QY 321 AAAGTAAAGAAAGTACTCAGGGATCTACTATGTGGGATATACAGCTCATCCTCCAG 380
DB 301 AAAGTAAAGAAAGTACTCAGGGATCTACTATGTGGGATATACAGCTCATCCTCCAG 360
QY 381 CAGCC 385
DB 361 CAGCC 365

RESULT S1
AWS12079/c

LOCUS AWS12079 369 bp mRNA linear EST 03-MAR-2000
DEFINITION xx70a08.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848982 3',
mRNA sequence.
ACCESSION AWS12079
VERSION AWS12079.1 GI:7150157
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 369)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/resources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 340.
Location/Qualifiers
1..369
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2848982"
/tissue_type="lymphoma, follicular mixed small and large
cell"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lym12"
/note="Organ: lymph node; Vector: pCMV-Sport6; Site 1:
SalI; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"

ORIGIN
Query Match 11.5%; Score 311; DB 2; Length 369;
Best Local Similarity 99.7%; Pred. No. 3e-124;
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2326 CAAACAAACAAACACCTGTGCTAGCTCAGTGCAGCTAAGATGAATCCCTACCAAC 2385
DB 362 CAAACAAACAAACACCTGTGCTAGCTCAGTGCAGCTAAGATGAATCCCTACCAAC 303
QY 2386 ACAGAGCTCACCATCTTATTAAGTGAAGAAACATGGGGAGGGGAAATGG 2445
DB 302 ACAGAGCTCACCATCTTATTAAGTGAAGAAACATGGGGAGGGGAAATGG 243
QY 2446 CTGCTTTGATATGTTCCCTGACCGATATCTTGAATGAGACCTCCATCAAGATGGA 2505
DB 242 CTGCTTTGATATGTTCCCTGACCGATATCTTGAATGAGACCTCCATCAAGATGGA 183
QY 2506 AAGTTGAAAACTTAATTAACAAATGCTTGTGGGCAAGATGGATTTGAGATTATCT 2565
DB 182 AAGTTGAAAACTTAATTAACAAATGCTTGTGGGCAAGATGGATTTGAGATTATCT 123
QY 2566 TCTCTCAGAAAGGCAATTTGAAGATTTGAGCAGATCTTCTCCCTAAGCAAAACCTT 2625
DB 122 TCTCTCAGAAAGGCAATTTGAAGATTTGAGCAGATCTTCTCCCTAAGCAAAACCTT 63
QY 2626 ATTGTAGTAAAAAGTCTTTTACTATCTTAATTAACAGATATTTGAGATTACATA 2685
DB 62 ATTGTAGTAAAAAGTCTTTTACTATCTTAATTAACAGATATTTGAGATTACATA 3
QY 2686 AA 2687
DB 2 AA 1

[illegible]

LOCUS	CD107362	506 bp	mRNA	linear	EST 15-MAY-2003
DEFINITION	AGENCOURT_14016621 NIH_MGC_179 Homo sapiens cDNA clone IMAGE:30368296 5', mRNA sequence.				
ACCESSION	CD107362				
VERSION	CD107362.1	GI:30760536			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 506)				
TITLE	NIH-MGC http://mgs.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapbs-remail.nih.gov				
	Tissue Procurement: Dr. Michael Brownstein				
	cDNA Library Preparation: Invitrogen Corp				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)				
	DNA Sequencing by: Agencourt Bioscience Corporation				
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:				
	http://image.lnl.gov				
	Plate: NDAM430 row: n column: 17				
	High quality sequence stop: 427.				
FEATURES	location/Qualifiers				
Source	1..506				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:30368296"				
	/tissue_type="Pituitary"				
	/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"				
	/note="NIH_MGC_179"				
	/note="Organ: brain; Vector: pCMV-Sport6.1; Site_1: EcoRV (destroyed); Site_2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC library."				
ORIGIN					
Query Match	11.4%; Score 307; DB 6; Length 506;				
Best Local Similarity	99.7%; Pred. No. 1.6e-122;				
Matches	357; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	976	AGATGAAAAATCCCACTCACTGCTCAAGATGCCAGACACCAAGGCTATTTGCTATG	10358		
DB	110	AGATGAAAAATCCCACTCACTGCTCAAGATGCCAGACACCAAGGCTATTTGCTATG	169		
QY	1036	AGATGTTATATAGACAGAGTGCATCCCTAGTCTGCTCAAAAAAACAATTC	10955		
DB	170	AGATGTTATATAGACAGAGTGCATCCCTAGTCTGCTCAAAAAAACAATTC	229		
QY	1096	TCGGCCCAAAACAATCAGAGAATTCAGATTGACTAGAAAATCAACAAGAA	11555		
DB	230	TCGGCCCAAAACAATCAGAGAATTCAGATTGACTAGAAAATCAACAAGAA	289		
QY	1156	TGAAGAACTGTAATCTTTTCCAGAGTAATATCTCTGATGCTTTCTTTAGATTAAAG	12151		
DB	290	TGAAGAACTGTAATCTTTTCCAGAGTAATATCTCTGATGCTTTCTTTAGATTAAAG	349		
QY	1216	TTCTGTAATTCATCACTGCTGGAATAATCTCTCAACCAAGAAGTTTATCACTTCAT	12751		
DB	350	TTCTGTAATTCATCACTGCTGGAATAATCTCTCAACCAAGAAGTTTATCACTTCAT	409		
QY	1276	CCCAAAATGGAATGGAATGTCAGCAAAACATATAAAAAAGTCTTAAAGATATCC	1333		
DB	410	CCCAAAATGGAATGGAATGTCAGCAAAACATATAAAAAAGTCTTAAAGATATCC	467		

RESULT 54
CD630758/c 280 bp mRNA linear EST 12-JAN-2004
LOCUS CD630758
DEFINITION 56071680H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD630758
VERSION CD630758.1 GI:40279024
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 280)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Genomics, Inc.
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com
Location/Qualifiers
1..280
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match 10.3%; Score 278; DB 6; Length 280;
Best Local Similarity 100.0%; Pred. No. 7.6e-110; Indels 0; Gaps 0;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1762 CAGATCTATATGAGACAGAAAGTGTGATGCGCCCAAGACAAAGACCTTCACCCAG 1821
DB CAGATCTATATGAGACAGAAAGTGTGATGCGCCCAAGACAAAGACCTTCACCCAG 221
QY 1822 GCTTCACTTATGACTTGTGCTGCAAAAAGTCTAGGTTTAAGGCTGTGCCGAAAC 1881
DB GCTTCACTTATGACTTGTGCTGCAAAAAGTCTAGGTTTAAGGCTGTGCCGAAAC 161
QY 220 GCTTCACTTATGACTTGTGCTGCAAAAAGTCTAGGTTTAAGGCTGTGCCGAAAC 161
DB 1882 CCATCCCAATTAAGAGACCGAGTCTGAAGTCACTTAATCTAGTAGAGAGACTTGG 1941
DB 160 CCATCCCAATTAAGAGACCGAGTCTGAAGTCACTTAATCTAGTAGAGAGACTTGG 101
QY 1942 AGTCAGGAGTGTGAGTGTGGGGACGCGGGGGCACTGGGTAACTTTAAAG 2001
DB 100 AGTCAGGAGTGTGAGTGTGGGGACGCGGGGGCACTGGGTAACTTTAAAG 41
QY 2002 TGGTTAATTCATTCATAGATATTTTAAAGAACTTAC 2039
DB 40 TGGTTAATTCATTCATAGATATTTTAAAGAACTTAC 3

RESULT 55
AM403028 282 bp mRNA linear EST 16-FEB-2000
LOCUS UI-HF-BKO-aal-c-09-0-UI.x1 NIH-MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3053944 5', mRNA sequence.
ACCESSION AM403028
VERSION AM403028.1 GI:6921844
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 282)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed By: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward

FEATURES
source
Location/Qualifiers
1..282
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3053944"
/issue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC 36"
/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI; constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match 10.2%; Score 275; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.6e-108; Indels 0; Gaps 0;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 CAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGAGGCTACTCCCTGAAGCTCAGC 320
DB CAAATCGTAATAGGAGAGAGTAGACTTCCAGATGAGAGGCTACTCCCTGAAGCTCAGC 67
QY 321 AAATGAAAGAAATAGTCAAGGATCTACTATGTGGGATATACAGCTCATCTCCAG 380
DB AAATGAAAGAAATAGTCAAGGATCTACTATGTGGGATATACAGCTCATCTCCAG 127
QY 381 CAGCCCTCACCAGAGAGTGTGCTGATGTCAGACACCTTCAAGCTTAAAGTC 440
DB CAGCCCTCACCAGAGAGTGTGCTGATGTCAGACACCTTCAAGCTTAAAGTC 187
QY 128 CAGCCCTCACCAGAGAGTGTGCTGATGTCAGACACCTTCAAGCTTAAAGTC 187
DB 441 ACCATGGGCTGACAGCAATAGATGACCTGTGTGACCAATCTGACATGCTGATG 500
QY 188 ACCATGGGCTGACAGCAATAGATGACCTGTGTGACCAATCTGACATGCTGATG 247
DB 501 GAACATGGGGAAGAGATGTGATTTTAACTTGA 535
QY 248 GAACATGGGGAAGAGATGTGATTTTAACTTGA 282

RESULT 56
A1651934/c 431 bp mRNA linear EST 17-DEC-1999
LOCUS WB51C08.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2309198 3'
DEFINITION similar to contains Alu repetitive element; contains element L1 L1
ACCESSION A1651934
VERSION A1651934.1 GI:4735913
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 431)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap/
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 www.bio.llnl.gov/bdrrp/image/image.html
 Insert Length: 543 Std Error: 0.00
 Seq primer: -40UP from Gldco.

FEATURES

source

1. .431
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2309198"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /clone_lib="NCI-CGAP GC6"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and 88 circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 10.1%; Score 273; DB 1; Length 431;

Best Local Similarity 99.7%; Pred. No. 1,1e-107;

Matches 323; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2379 TACCAACAGAGAGTCACTCTTACTTAAGTAAACATGGGGAAGG 2438
 328 TACCAACAGAGAGTCACTCTTACTTAAGTAAACATGGGGAAGG 269
 2439 GGAATGGCTGTTTGAATGTTCCCTGACGATATCTTGAATGAGACCTCCCTACCA 2498
 268 GGAATGGCTGTTTGAATGTTCCCTGACGATATCTTGAATGAGACCTCCCTACCA 209
 2499 GTGATGAAGTGTGAAGAACTTAATCAAACTCTTGGGCAAGATGGATTGAGG 2558
 208 GTGATGAAGTGTGAAGAACTTAATCAAACTCTTGGGCAAGATGGATTGAGG 149
 2559 ATTATCTTCTCTGGAAGGATGTGAAGGATTTGAGCCGATCTCTCCCTACTGCA 2618
 148 ATTATCTTCTCTGGAAGGATGTGAAGGATTTGAGCCGATCTCTCCCTACTGCA 89
 2619 AAACCTTATTTAGTAAAGTCTTCTTACTTAAATTAAGATATTTGAGAT 2678
 88 AAACCTTATTTAGTAAAGTCTTCTTACTTAAATTAAGATATTTGAGAT 29
 2679 TCACATATAAAAAAAAAAAAAA 2702
 28 TCACATATAAAAAAAAAAAAAA 5

RESULT 57

AA604443/c 332 bp mRNA linear EST 08-OCT-1997

LOCUS np57904.r1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1130454 5'

DEFINITION similar to confamil Alu repetitive element; mRNA sequence.

ACCESSION AA604443

VERSION AA604443.1 GI:2445352

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 332)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

www.bio.llnl.gov/bdrrp/image/image.html

Insert Length: 492 Std Error: 0.00

Seq primer: -28m13 rev1 ET from Amersham.

Location/Qualifiers

1. .332

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1130454"

/sex="female, pooled"

/tissue_type="breast"

/lab_host="DH10B"

/clone_lib="NCI CGAP Br2"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I -

oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned

into the Not I and Eco RI sites of the modified pT73

vector. This library is the normalized version of

NCI CGAP Br1.1. Library was constructed by Bento Soares

and M. Fatima Bonaldo."

ORIGIN

Query Match 10.1%; Score 272; DB 1; Length 332;

Best Local Similarity 99.7%; Pred. No. 3,1e-107;

Matches 322; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2268 GCTGAGTGGCACCACCTGACCTCCGCTTAGGAGCAAGGCAAACTCCATACCAACA 2327
 323 GCTGAGTGGCACCACCTGACCTCCGCTTAGGAGCAAGGCAAACTCCATACCAACA 264
 2328 AACAAACAAACACCTGTAGTCACTGACGCTAAGATGACATCCCTCAACAC 2387
 263 AACAAACAAACACCTGTAGTCACTGACGCTAAGATGACATCCCTCAACAC 204
 2388 AGAGCTCACCATCTTTATCTTAAGTAAACATGGGGAAGGGAATGGCT 2447
 203 AGAGCTCACCATCTTTATCTTAAGTAAACATGGGGAAGGGAATGGCT 144
 2448 GCTTTGATATATGTTCCCTGACGATATCTTGAATGAGACCTCCCTACCAAGATGA 2507
 143 GCTTTGATATATGTTCCCTGACGATATCTTGAATGAGACCTCCCTACCAAGATGA 84
 2508 GTGTTGAAAACTTAATTAACAAATGCTTTGGGCAAGATGAGATTATCTTC 2567
 83 GTGTTGAAAACTTAATTAACAAATGCTTTGGGCAAGATGAGATTATCTTC 24
 2568 TCTCAGAAAGGCAATTGTGAAGA 2590
 23 TCTCAGAAAGGCAATTGTGAAGA 1

RESULT 58

AM138797/c 557 bp mRNA linear EST 29-OCT-1999

LOCUS AM138797

DEFINITION UI-H-B1-aep-d-12-0-UI.a1 NCI CGAP_Sub3 Homo sapiens cDNA clone

IMAGE:2719943 3', mRNA sequence.

ACCESSION AM138797

Query Match 9.4%; Score 255; DB 5; Length 774;
 Best Local Similarity 100.0%; Pred. No. 7.3e-100;
 Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 558 GAGTCCCATATATGGGTCATCTCTCCCATCTCTCGAGATGGGAGAAAGTATATGACC 617
 DB 1 GAGTCCCATATATGGGTCATCTCTCCCATCTCTCGAGATGGGAGAAAGTATATGACC 60
 QY 618 TTTCATCTGGGTCGAGAAACCTGTGAGAGAACTTCTCAAGCCCATCTTGTGACG 677
 DB 61 TTTCATCTGGGTCGAGAAACCTGTGAGAGAACTTCTCAAGCCCATCTTGTGACG 120
 QY 678 AAGCTCTGTGAAGTGTCTGTATGACCCAGATTTCTTCATGCTCTGTGCTCTG 737
 DB 121 AAGCTCTGTGAAGTGTCTGTATGACCCAGATTTCTTCATGCTCTGTGCTCTG 180
 QY 738 TTGGTCCCTCTCTGCTCACTCTTTTGTATCTGGGCTATTTTGTGTTTCTGAAGA 797
 DB 181 TTGGTCCCTCTCTGCTCACTCTTTTGTATCTGGGCTATTTTGTGTTTCTGAAGA 240
 QY 798 GAGAGACAAGAGAG 812
 DB 241 GAGAGACAAGAGAG 255

RESULT 62

LOCUS CB046322 631 bp mRNA linear EST 17-JAN-2003
 DEFINITION NISC_gtf03g04.v1 NCI_CGAP_Kid12 Homo sapiens cDNA clone
 CB046322
 IMAGE:3352678 5', mRNA sequence.

ACCESSION CB046322
 VERSION CB046322.1 GI:27784609
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 COMMENT Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 CDNA Library Preparation:
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 info@image.llnl.gov
 Plate: LLM7959 row: N column: 7
 Seq primer: M13R1 reverse primer (ABI).
 Location/Qualifiers

FEATURES

source

1..631
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3352678"
 /tissue_type="2 pooled tumors (clear cell type)"
 /lab_host="DH10B"
 /note="Organ: Kidney; Vector: pRTT3D-Pac (Pharmacia) with
 a modified polylinker; Site1: Not 1; Site2: Eco RI;
 Plasmid DNA from the normalized library NCI_CGAP_Kid12 was
 prepared, and 86 circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (cloneids 1323912-1325831, 1471368-1472903 and
 1492104-1493255). Subtraction by Bento Soares and M.
 Fatima Bonaldo."

ORIGIN

Query Match 9.3%; Score 252; DB 6; Length 631;
 Best Local Similarity 100.0%; Pred. No. 1.5e-98;
 Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 417 GAGCCTGTCAAGCCTTAAGTCAACATGGGCTGTGACAGAGCAATTAAGTGGACCTGT 476
 DB 99 GAGCCTGTCAAGCCTTAAGTCAACATGGGCTGTGACAGAGCAATTAAGTGGACCTGT 158
 QY 477 GTGACCAATCTGACATGCTGCAATGGAACATGGGAGAGAGATATTAATCTCGAAG 536
 DB 159 GTGACCAATCTGACATGCTGCAATGGAACATGGGAGAGAGATATTAATCTCGAAG 218
 QY 537 GCCCTGGGCAAGCAGCAATGATGCCATATAGGATGATGATGATGATGATGATGATG 596
 DB 219 GCCCTGGGCAAGCAGCAATGATGCCATATAGGATGATGATGATGATGATGATGATG 278
 QY 597 TGGGAGAAAGTATATGACCTTCACTGCGTTGCCAGGAACTGTGACAGAACTTC 656
 DB 279 TGGGAGAAAGTATATGACCTTCACTGCGTTGCCAGGAACTGTGACAGAACTTC 338
 QY 657 TCAAGCCCATC 668
 DB 339 TCAAGCCCATC 350

RESULT 63

LOCUS A1289790/c 354 bp mRNA linear EST 21-DEC-1998
 DEFINITION gw1b12.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:1990847 3'
 similar to contatns element L1 repetitive element ;, mRNA sequence.
 A1289790
 VERSION A1289790.1 GI:3931631
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

LOCUS A1289790/c 354 bp mRNA linear EST 21-DEC-1998
 DEFINITION gw1b12.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:1990847 3'
 similar to contatns element L1 repetitive element ;, mRNA sequence.
 A1289790
 VERSION A1289790.1 GI:3931631
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 COMMENT Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www.bio.llnl.gov/bbrp/image/image.html
 Insert Length: 273 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 333.
 Location/Qualifiers

FEATURES

source

1..354
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1990847"
 /tissue_type="poorly-differentiated endometrial
 adenocarcinoma, 2 pooled tumors"
 /lab_host="DH10B"
 /clone="NCI_CGAP_Ut3"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.45 kb. Life Technologies catalog #:
 11541-018"

ORIGIN

Query Match 9.2%; Score 250; DB 1; Length 354;
 Best Local Similarity 99.7%; Pred. No. 1.2e-97;
 Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2381 CCAACACAGAGCTCACCATCTCTTACTTAACTTAAGTGAAGAAAACATGGGAGGGAAGGGG 2440
 DB 313 CCAACACAGAGCTCACCATCTCTTACTTAACTTAAGTGAAGAAAACATGGGAGGGAAGGGG 254

QY 2441 AATGGCTGCTTTGATATGTTCCCTGACGCAATCTTGAATGAGAGCTCCCTACCAAGT 2500
 DB 253 AATGGCTGCTTTGATATGTTCCCTGACCAATCTTGAATGAGAGCTCCCTACCAAGT 194

QY 2501 GATGAAGGTGTGAAAACTTAATACAAATGCTTGTGGCAAGATGGAGATTGAGAT 2560
 DB 193 GATGAAGGTGTGAAAACTTAATACAAATGCTTGTGGCAAGATGGAGATTGAGAT 134

QY 2561 TATCTTCTTCAGAAAGGCATTGTGAAGAAATGAGCAATCTCTCCCTACTGCAG 2620
 DB 133 TATCTTCTTCAGAAAGGCATTGTGAAGAAATGAGCAATCTCTCCCTACTGCAG 74

QY 2621 ACCCTATTGATGAAAAAGCTCTTCTTACTATCTTAATAAAGATATTGTGAGATTC 2680
 DB 73 ACCCTATTGATGAAAAAGCTCTTCTTACTATCTTAATAAAGATATTGTGAGATTC 14

QY 2681 A 2681
 DB 13 A 13

RESULT 64
 AI521522/c 321 bp mRNA linear EST 12-MAY-1999
 LOCUS t064b07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2183029 3'
 DEFINITION Similar to contains element MER6 MER6 repetitive element ;, mRNA
 sequence.
 ACCESSION AI521522
 VERSION AI521522.1 GI:4435657
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 321)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Mookajuk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 728 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 295
 POLYA-No.

FEATURES
 source Location/Qualifiers

1..321
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2183029"
 /tissue_type="poorly differentiated adenocarcinoma with
 signed ring cell features"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP Gas4"
 /note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 catalog #: 11502-010"

Query Match 9.2%; Score 249; DB 1; Length 321;
 Best Local Similarity 99.7%; Pred. No. 3.4e-97;
 Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

QY 2381 CCAACACAGAGCTCACCATCTCTTACTTAACTTAAGTGAAGAAAACATGGGAGGGAAGGGG 2440
 DB 321 CCAACACAGAGCTCACCATCTCTTACTTAACTTAAGTGAAGAAAACATGGGAGGGAAGGGG 262

QY 2441 AATGGCTGCTTTGATATGTTCCCTGACGCAATCTTGAATGAGAGCTCCCTACCAAGT 2500
 DB 261 AATGGCTGCTTTGATATGTTCCCTGACCAATCTTGAATGAGAGCTCCCTACCAAGT 202

QY 2501 GATGAAGGTGTGAAAACTTAATACAAATGCTTGTGGCAAGATGGAGATTGAGAT 2560
 DB 201 GATGAAGGTGTGAAAACTTAATACAAATGCTTGTGGCAAGATGGAGATTGAGAT 142

QY 2561 TATCTTCTTCAGAAAGGCATTGTGAAGAAATGAGCAATCTCTCCCTACTGCAG 2620
 DB 141 TATCTTCTTCAGAAAGGCATTGTGAAGAAATGAGCAATCTCTCCCTACTGCAG 82

QY 2621 ACCCTATTGATGAAAAAGCTCTTCTTACTATCTTAATAAAGATATTGTGAGATTC 2680
 DB 81 ACCCTATTGATGAAAAAGCTCTTCTTACTATCTTAATAAAGATATTGTGAGATTC 22

RESULT 65
 AM080386/c 315 bp mRNA linear EST 14-OCT-1999
 LOCUS x641e10.x1 NCI_CGAP_Bso2 Homo sapiens cDNA clone IMAGE:2610474 3'
 DEFINITION mRNA sequence.
 ACCESSION AM080386
 VERSION AM080386
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 315)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip
 Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40UP from Gibco
 High quality sequence stop: 309.

FEATURES
 source Location/Qualifiers

1..315
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2610474"
 /tissue_type="squamous cell carcinoma"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP Bso2"
 /note="Organ: esophagus; Vector: pCMV-SPORT6; Site 1:
 SalI; Site 2: NotI; Cloned unidirectionally. Primer:
 Oligo dt. Average insert size 1.1 kb. Life Technologies
 catalog #: 11502-010"

ORIGIN

Query Match	9.1%	Score 247;	DB 2;	Length 315;
Best Local Similarity	100.0%	Pred. No. 2.5e-96;		
Matches 247;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1610	CCTCATGAAATTGGCTCCAAATGAACTACTATTTCATAGACATTGTAGCAGGCTGA	1663
Db	315	CCTCATGAAATTGGCTCCAAATGAACTACTATTTCATAGACATTGTAGCAGGCTGA	256
Qy	1670	CCACGATTTCCAGAGGGCCAGGTGTGATCCACAGACCTTGAAGGTCAAAGTTACAAA	1728
Db	255	CCACGATTTCCAGAGGGCCAGGTGTGATCCACAGACCTTGAAGGTCAAAGTTACAAA	196
Qy	1720	GATGAAGATCAGGGTAGCTGACCATGTTTGGCACTACTTAATGAGACACAGAACTG	1789
Db	195	GATGAAGATCAGGGTAGCTGACCATGTTTGGCACTACTTAATGAGACACAGAACTG	136
Qy	1790	TGCATGCCCCAAGACCAAGACCTTCACAGCCAGCTTCATTATGACCTTGTGCTGCAAA	1849
Db	135	TGCATGCCCCAAGACCAAGACCTTCACAGCCAGCTTCATTATGACCTTGTGCTGCAAA	76
Qy	1850	GAAAAGT 1856	
Db	75	GAAAAGT 69	

RESULT 66	
AM379005/c	
LOCUS	AM379005 493 bp mRNA linear EST 04-FEB-2000
DEFINITION	RC3- <i>HT0230</i> -241099-012-b08 <i>HT0230</i> Homo sapiens cDNA, mRNA sequence.
ACCESSION	AM379005
VERSION	AM379005.1 GI:6883664
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 493)
TITLE	HCGP http://www.ludwig.org.br/ORESTES .
JOURNAL	The FAPESP/LICR Human Cancer Genome Project
COMMENT	Unpublished (1999) Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<a href="http://www.ludwig.org.br/scripts/gethtml2.pl?l1=RC3&t2=RC3-<i>HT0230</i>-241099-012-b08&t3=1999-10-24&t4=1">http://www.ludwig.org.br/scripts/gethtml2.pl?l1=RC3&t2=RC3-<i>HT0230</i>-241099-012-b08&t3=1999-10-24&t4=1) Seq primer: puc 18 forward High quality sequence start: 14 High quality sequence stop: 492. Location/Qualifiers

FEATURES	
source	1..493
	organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/dev_stage="Adult"
	/clone_id="HT0230"
	/note="Organ: head neck; Vector: puc18; Site 1: Smal; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN	
Query Match	9.1%; Score 245; DB 2; Length 493;
Best Local Similarity	99.4%; Pred. No. 1.8e-95;

Matches	465; Conservative	0; Mismatches	2; Indels	1; Gaps	1;
QY	1314	AAAGTCTTGAAGATATTCCTATTGAAATGTAATGCAAGCTCACACATATTATATGACAG	1373		
Db	472	AAAGTCTTGAAGATATTCCTATTGAAATGTAATGCAAGCTCACACATATTATATGACAG	413		
QY	1374	CCTGTGTGTAATTAATGATGGCTCCAGGTCAGTGTCTGAGTTTGATTCATTCACAGGGCTT	1433		
Db	412	CCTGTGTGTAATTAATGATGGCTCCAGGTCAGTGTCTGAGTTTGATTCATTCACAGGGCTT	353		
QY	1434	GGATGTCCAGATTTATACCAAGAGTCTTGTCTACCGAGGCGCAAGAACCAACAAACAGACA	1493		
Db	352	GGATGTCCAGATTTATACCAAGAGTCTTGTCTACCGAGGCGCAAGAACCAACAAACAGACA	293		
QY	1494	GACAAATGTCAG-CGAAAGCCAGATGCACCTGACAAATAATGATGTATTATTTGGCTCTATA	1552		
Db	292	GACAAATGTCAGCCGAAAGCAGATGCACCTGACAAATAATGATGTATTATTTGGCTCTATA	233		
QY	1553	AACATATGCCCACACATATGCTGAGCTTACATTAATTTGGTCAGAGCTGCTGTGCTCCCT	1612		
Db	232	AACATATGCCCACACATATGCTGAGCTTACATTAATTTGGTCAGAGCTGCTGTGCTCCCT	173		
QY	1613	CATGAAATTTGGCTCCCAATGAATGAATGAACTACTTTTCATGAGCAGTGTGTAGCAGGCTGACCA	1672		
Db	172	CATGAAATTTGGCTCCCAATGAATGAATGAACTACTTTTCATGAGCAGTGTGTAGCAGGCTGACCA	113		
QY	1673	CAGATTTCCCGAGGGCCAGGTGTGGATCCACAGAGCTTGAAGGTCAAAGTTCAACAAAGAT	1732		
Db	112	CAGATTTCCCGAGGGCCAGGTGTGGATCCACAGAGCTTGAAGGTCAAAGTTCAACAAAGAT	53		
QY	1733	GAAATATCAGGGTGTGCTGACCATGTTTGGAGATCTACTATTAATGGAGAC	1780		
Db	52	GAAATATCAGGGTGTGCTGACCATGTTTGGAGATCTACTATTAATGGAGAC	5		
RESULT 67					
AA554342/c					
LOCUS	AA554342	411 bp	mRNA	linear	EST 09-SEP-1997
DEFINITION	nl03e08.s1 NCI_CGAP_Co3 Homo sapiens CDNA clone IMAGE:1029254 3',				
ACCESSION	AA554342				
VERSION	AA554342.1	GI:2324881			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 411)				
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.				
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				
	Unpublished (1997)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapbs-remail.nih.gov				
	Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,				
	M.D., Ph.D.				
	CDNA Library Preparation: M. Bento Soares, Ph.D.				
	CDNA Library Arraying: Greg Lennon, Ph.D.				
	DNA Sequencing by: Washington University Genome Sequencing Center				
	Clone distribution: NCI-CGAP clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LUNL at:				
	www-bio.llnl.gov/bdrip/image/image.html				
	Insert Length: 579 Std Error: 0.00				
	Seq primer: -40ml3 fwd. ET from Amersham				
	High quality sequence stop: 388.				
FEATURES					
SOURCE	Location/Qualifiers				
	1. 411				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:1029254"				
	/sex="pooled"				
	/tissue_type="colon"				

poly(A) linker site. 1: Ecor I; Site 2: NotI; tissues: Chondritic mucosa with Crohn's disease, Chondritic mucosa with ulcerative colitis, Perit lymphus, Cervix, Cervical adenocarcinoma, Bladder carcinoma, Ligament cells, Prostate carcinoma, Bladder carcinoma, Brain oligodendrocytes; NCI_CGAP_Sub0 is a subcloned cDNA library constructed according to Bonaldi, Lemmon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a NotI site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with NotI, and cloned directionally into pTRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the NotI site and the (GT)₁₈ tail. The sequence tags for this library are GCTC, AGC, GGAGC, GGAG, TACC, TACC, ATGC, AGCA, ATAC. For additional information, contact: Bento Soares, bento-soares@iowa.edu TAG_LIB=UI-H-CCO TAG_SEQ=CGAG-

Site 2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life Technologies."

ORIGIN

Query Match 7.5%; Score 204; DB 5; Length 466;
Best Local Similarity 99.6%; Pred. No. 1,4e-77;
Matches 254; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1784 GAAGTGTGATGGCCCAAGACAGACGACCTTCACGCGCTTCATTATGACCTTGTCT 1843
1 GAAGTGTGATGGCCCAAGACAGACGACCTTCACGCGCTTCATTATGACCTTGTCT 60
Qy 1844 GCAAAAGAAAGTGTAGATTTTAAAGCTGTGCGCAGAACCCATCCCAATTAAGAGACGAG 1903
61 GCAAAAGAAAGTGTAGATTTTAAAGCTGTGCGCAGAACCCATCCCAATTAAGAGACGAG 120
Db 1904 TCTGAAGTCACTTGTAAATCTAGTGTAGAGAGACTTGAGAGTCAAGGAGTGTGTG 1963
121 TCTGAAGTCACTTGTAAATCTAGTGTAGAGAGACTTGAGAGTCAAGGAGTGTGTG 180
Qy 1964 GGCACGGGGGGGCGAGTGGTACTTGTAAACCTTTAAAGTGTATTCATTCAATAGATA 2023
181 GGCACGGGGGGGCGAGTGGTACTTGTAAACCTTTAAAGTGTATTCATTCAATAGATA 240
Db 2024 TTTATTAAAGACCTA 2038
Qy 241 TTTATTAAAGACCTA 255

RESULT 72

BM551726 1026 bp mRNA linear EST 20-FEB-2002
LOCUS BM551726
DEFINITION AGENCOURT_6544759 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548139
5', mRNA sequence.

ACCESSION BM551726 GI:18788997
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC/DBT/DTP
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.lnl.gov
Plate: LAM1256 row: j column: 12
High quality sequence stop: 552.

FEATURES

Source

1. 1026
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5548139"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 7.5%; Score 202; DB 4; Length 1026;

Best Local Similarity 99.6%; Pred. No. 9.2e-77;
Matches 252; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1786 AGTGTGATGGCCCAAGACAGACGACCTTCACGCGCTTCATTATGACCTTGTCTGC 1845
1 AGTGTGATGGCCCAAGACAGACGACCTTCACGCGCTTCATTATGACCTTGTCTGC 60
Db 1846 AAAAGAAAGTGTAGATTTTAAAGCTGTGCGCAGAACCCATCCCAATTAAGAGACGAGTC 1905
61 AAAAGAAAGTGTAGATTTTAAAGCTGTGCGCAGAACCCATCCCAATTAAGAGACGAGTC 120
Qy 1906 TGAAGTCACTTGTAAATCTAGTGTAGAGAGACTTGAGAGTCAAGGAGTGTGTG 1965
121 TGAAGTCACTTGTAAATCTAGTGTAGAGAGACTTGAGAGTCAAGGAGTGTGTG 180
Db 1966 CACGGGGGGGCGAGTGGTACTTGTAAACCTTTAAAGTGTATTCATTCAATAGATATT 2025
181 CACGGGGGGGCGAGTGGTACTTGTAAACCTTTAAAGTGTATTCATTCAATAGATATT 240
Qy 2026 TATTAAAGACCTA 2038
Db 241 TATTAAAGACCTA 253

RESULT 73

AA381714 321 bp mRNA linear EST 21-APR-1997
LOCUS AA381714
DEFINITION EST94847 Activated T-cells 1 Homo sapiens cDNA 5' end, mRNA
sequence.

ACCESSION AA381714 GI:2034053
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,
Bult C.J., Lee N.H., Kirkness E.F., Winesock K.G., Gocayne J.D.,
White O., Sutton G., Blake J.A., Brannon R.C., Man-Mai C.,
Clayton R.A., Cline T.R., Cotton M.D., Earle-Hughes J., Fine L.D.,
Fitzgerald L.M., Fitzhugh W.M., Fritchman J., Geoghagen N.S.,
Giordak A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle P.S., Jr.,
Kelly J.M., Kelley J.C., Liu L.-I., Marmore S.M., Merrick J.M.,
Moreno-Palauques R.F., McDonald L.A., Nguyen D.T., Pelligriano S.M.,
Phillips C.A., Ryder S.E., Scott U.L., Saudex D.M., Shirley R.,
Small K.V., Spriggs T.A., Utterback T.R., Weidman J.F., Li Y.,
Bednarek D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.J.,
Dinko D., Feng D.-F., Ferris A., Fischer C., Hastings G.A.,
He W.W., Hu J.S., Greene J.M., Gruber J., Hudson P., Kim A.K.,
Kozak D.L., Kunsch C., Hungjun J., Li H., Weisner P.S., Olsen H.,
Raymond L., Wei Y.F., Wang J., Xu C., Yu G.L., Ruben S.M.,
Dillon P.J., Pannon M.R., Rosen C.A., Haseltine W.A., Fields C.,
Fraser C.M. and Venter J.C.
TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
PUBMED 7560608

COMMENT

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/cdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
1. 321
/organism="Homo sapiens"

FEATURES

Source

ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 7.2%; Score 194; DB 1; Length 294;

Best Local Similarity 100.0%; Pred. No. 3.3e-73; Indels 0; Gaps 0;

Matches 194; Conservative 0; Mismatches 0;

Qy	2487	CCTCCCTACCAAGTATGAAAGTGTGAAAACTTAATAACAATGCTGTGGCAAGA	2546
Db	223	CTCCCTACCAAGTATGAAAGTGTGAAAACTTAATAACAATGCTGTGGCAAGA	164
Qy	2547	ATGGGATTGAGATTATCTCTCTCAGAAAAGCATTGTGAAGAAATTGAGCCAGATCTT	2606
Db	163	ATGGGATTGAGATTATCTCTCTCAGAAAAGCATTGTGAAGAAATTGAGCCAGATCTT	104
Qy	2607	CTCCCTACCAAAACCTATTGTAGTAAAAAGTCTTTACTATCTTAATAAACAG	2666
Db	103	CTCCCTACCAAAACCTATTGTAGTAAAAAGTCTTTACTATCTTAATAAACAG	44
Qy	2667	ATATTGTGAGATTC	2680
Db	43	ATATTGTGAGATTC	30

Search completed: October 28, 2004, 19:18:41
Job time : 8276 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 13:09:00 ; Search time 223 Seconds

(without alignments)
8618.714 Million cell updates/sec

Title: US-09-745-605-1

Perfect score: 2704
Sequence: 1 ggaagcgcctcatcttcagc.....aaaaaaaaaaaaaaaaaaaaa 2704

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 35539441 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

Issued Patents NA: *
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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTCTUS.COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	649	24.0	921	4 US-09-023-655-401	Sequence 401, App
2	281	10.4	344	4 US-09-513-999C-395	Sequence 395, App
3	182	6.7	435	4 US-09-513-999C-21312	Sequence 21312, A
4	61	2.3	10684	3 US-08-618-1008-3	Sequence 3, Appli
5	59	2.2	73	3 US-09-506-729-85	Sequence 55, Appli
6	59	2.2	394	4 US-09-621-976-8541	Sequence 8541, App
7	59	2.2	807	2 US-08-531-9278-9	Sequence 9, Appli
8	59	2.2	1776	2 US-08-531-9278-9	Sequence 1, Appli
9	59	2.2	1776	4 US-09-041-886-12	Sequence 12, Appli
10	59	2.2	8981	4 US-09-526-193A-20	Sequence 20, Appli
11	59	2.2	63000	4 US-08-780-172-18	Sequence 18, Appli
12	58	2.1	330	3 US-09-078-294-74	Sequence 24, Appli
13	58	2.1	2749	3 US-10-140-002-585	Sequence 385, App
14	58	2.1	11811	3 US-09-008-294-7	Sequence 7, Appli
15	58	2.1	13865	3 US-09-009-217-11	Sequence 11, Appli
16	58	2.1	13865	4 US-09-009-656-11	Sequence 11, Appli
17	58	2.1	13865	4 US-09-054-272-11	Sequence 11, Appli
18	58	2.1	90541	4 US-09-759-359A-3	Sequence 3, Appli
19	58	2.1	90541	4 US-10-207-973-3	Sequence 3, Appli
20	58	2.1	111282	3 US-09-754-250-3	Sequence 3, Appli
21	57	2.1	688	1 US-08-599-252-04	Sequence 94, Appli
22	57	2.1	688	5 PCT-US96-06352-94	Sequence 94, Appli
23	57	2.1	688	5 PCT-US96-06583-94	Sequence 94, Appli
24	57	2.1	66933	4 US-09-544-398B-11	Sequence 11, Appli
25	57	2.1	66933	4 US-09-543-771-11	Sequence 11, Appli
26	57	2.1	72049	4 US-09-544-398B-9	Sequence 9, Appli
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28	2.1	153	4 US-09-513-999C-35299	Sequence 35299, A
29	2.0	2480	3 US-09-534-638-3	Sequence 3, Appli
30	2.0	473	4 US-09-621-976-691	Sequence 691, App
31	2.0	44848	4 US-09-435-739-42	Sequence 42, Appli
32	2.0	44848	4 US-09-988-113-42	Sequence 42, Appli
33	2.0	786431	4 US-09-751-389-3	Sequence 3, Appli
34	2.0	8353	3 US-08-611-587-1	Sequence 1, Appli
35	2.0	116592	4 US-09-818-512-3	Sequence 3, Appli
36	1.9	49312	4 US-09-671-317-485	Sequence 485, App
37	1.9	118067	4 US-09-497-855A-32	Sequence 32, Appli
38	1.8	297	4 US-09-621-976-12888	Sequence 12888, A
39	1.8	307	4 US-09-621-976-9714	Sequence 9714, Ap
40	1.8	369	4 US-09-783-203-1	Sequence 1, Appli
41	1.8	15418	4 US-09-994-427A-1	Sequence 1, Appli
42	1.8	15418	4 US-09-244-438-1	Sequence 1, Appli
43	1.8	15418	4 US-09-244-438-1	Sequence 1, Appli
44	1.8	29485	4 US-09-785-381-6	Sequence 6, Appli
45	1.8	191	4 US-09-513-999C-30096	Sequence 30096, A
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47	1.8	511	4 US-09-621-976-1354	Sequence 1354, Ap
48	1.8	6769	1 US-08-480-784-20	Sequence 20, Appli
49	1.8	6769	1 US-08-483-553-20	Sequence 20, Appli
50	1.8	6769	1 US-08-487-002-20	Sequence 20, Appli
51	1.8	6769	1 US-08-483-554B-20	Sequence 20, Appli
52	1.8	6769	1 US-08-488-011B-20	Sequence 20, Appli
53	1.8	6769	3 US-08-850-727-20	Sequence 20, Appli
54	1.8	6769	5 PCT-US95-10202-20	Sequence 20, Appli
55	1.8	6769	5 PCT-US95-10203-20	Sequence 20, Appli
56	1.8	6769	5 PCT-US95-10220-20	Sequence 20, Appli
57	1.8	8174	1 US-07-914-281-5	Sequence 5, Appli
58	1.8	8174	1 US-08-393-246-5	Sequence 5, Appli
59	1.8	8174	1 US-08-525-058A-5	Sequence 5, Appli
60	1.8	8174	2 US-08-686-731-5	Sequence 5, Appli
61	1.8	8174	3 PCT-US91-00899-3	Sequence 3, Appli
62	1.8	8174	5 PCT-US91-00899-3	Sequence 3, Appli
63	1.8	162440	3 US-09-345-882-1	Sequence 1, Appli
64	1.8	141	4 US-09-513-999C-20281	Sequence 20281, A
65	1.8	2713	2 US-08-916-901-6	Sequence 6, Appli
66	1.8	2713	3 US-09-154-602-6	Sequence 6, Appli
67	1.8	26928	4 US-09-054-772-41	Sequence 41, Appli
68	1.8	72928	3 US-09-009-913-1	Sequence 1, Appli
69	1.8	107820	4 US-09-792-616-1	Sequence 1, Appli
70	1.8	114793	4 US-10-148-806-3	Sequence 3, Appli
71	1.7	274	4 US-09-513-999C-17885	Sequence 17885, A
72	1.7	280	2 US-08-849-701-7	Sequence 7, Appli
73	1.7	283	1 US-08-133-629-8	Sequence 8, Appli
74	1.7	283	4 US-08-579-445-26	Sequence 26, Appli
75	1.7	330	4 US-09-513-999C-27220	Sequence 27220, A
76	1.7	339	4 US-09-513-999C-22312	Sequence 22312, A
77	1.7	526	4 US-08-579-445-24	Sequence 24, Appli
78	1.7	4080	2 US-08-710-249-3	Sequence 3, Appli
79	1.7	4080	3 US-09-220-157A-3	Sequence 3, Appli
80	1.7	6063	1 US-08-195-744-4	Sequence 4, Appli
81	1.7	6063	2 US-08-788-879-4	Sequence 4, Appli
82	1.7	29485	4 US-09-785-381-6	Sequence 6, Appli
83	1.7	29629	4 US-09-729-895-3	Sequence 3, Appli
84	1.7	29629	4 US-10-135-689-3	Sequence 3, Appli
85	1.7	48763	4 US-09-916-204-3	Sequence 3, Appli
86	1.7	48763	4 US-10-282-048-3	Sequence 3, Appli
87	1.7	50000	3 US-09-146-053-3	Sequence 3, Appli
88	1.7	55298	4 US-09-491-356C-1	Sequence 1, Appli
89	1.7	56516	2 US-08-996-306-1	Sequence 1, Appli
90	1.7	56516	3 US-09-318-307-1	Sequence 1, Appli
91	1.7	56516	3 US-09-318-307-1	Sequence 1, Appli
92	1.7	56520	3 US-09-338-907-179	Sequence 179, App
93	1.7	66200	3 US-09-218-207-179	Sequence 179, App
94	1.7	62804	3 US-10-800-960-3	Sequence 3, Appli
95	1.7	62804	4 US-10-096-960-3	Sequence 3, Appli
96	1.7	99916	4 US-09-816-095-3	Sequence 3, Appli
97	1.7	106746	4 US-09-326-402C-1	Sequence 1, Appli
98	1.7	106746	4 US-09-326-402C-12	Sequence 12, Appli
99	1.7	118067	4 US-09-497-855A-32	Sequence 32, Appli
100	1.7	168575	4 US-09-426-290-1	Sequence 1, Appli

ALIGNMENTS

```
RESULT 1
US-09-023-655-401
; Sequence 401, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 401:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THP1PLB02
; CLONE: 156352
; US-09-023-655-401

Query Match      24.0%; Score 649; DB 4; Length 921;
Best Local Similarity 99.8%; Pred. No. 2.4e-269;
Matches 819; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1220 TAATTCATCCACTGCTGGAAGAAATCTCTCAAAACCCAGAAAGTTTATCATCTTCAATCCA 1279
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DB 99 TAATTCATCCACTGCTGGAAGAAATCTCTCAAAACCCAGAAAGTTTATCATCTTCAATCCA 158

QY 1280 AAAATGGATTGTGATGTACAGCAACATATAAAAAAGTCTAGAGATTCTCTATAGA 1339
    |||
DB 159 AAAATGGATTGTGATGTACAGCAACATATAAAAAAGTCTAGAGATTCTCTATAGA 218

QY 1340 AATGTAATGCAAGTTCACACATATTATATGACAGCTGTGTATTAATGATGGCTCCAG 1399
    |||
DB 219 AATGTAATGCAAGTTCACACATATTATATGACAGCTGTGTATTAATGATGGCTCCAG 278

QY 1400 TCAGTGTCTGAGTTTCATTCATCCAGAGGCTTGATGATGATTAATACCAAGTCT 1459
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DB 279 TCAGTGTCTGAGTTTCATTCATCCAGAGGCTTGATGATGATTAATACCAAGTCT 338
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QY 1460 TGTACCCAGAGGCGCAAGAACCAAAAAGAGACAGACAGATCTCAGCAGAGCAGATGAC 1519
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DB 339 TGTACCCAGAGGCGCAAGAACCAAAAAGAGACAGACAGATCTCAGCAGAGCAGATGAC 398

QY 1520 CTGACAAAAATGATGTATTAATTTGGCTCTATTAACCTATATGCTCCAGACATATGCTGAC 1579
    |||
DB 399 CTGACAAAAATGATGTATTAATTTGGCTCTATTAACCTATATGCTCCAGACATATGCTGAC 458

QY 1580 TTACACTAATTGTGTAGACGTCTGTGCTCCCTCATGAAATGGCTCCAAATGAATGAC 1639
    |||
DB 459 TTACACTAATTGTGTAGACGTCTGTGCTCCCTCATGAAATGGCTCCAAATGAATGAC 518

QY 1640 TAC-TTTTATGAGCAGTTGTGTAGCAGGCTGACCAAGATTTCCAGAGGCGCAGTGTGGA 1698
    |||
DB 519 TACTTTATGAGCAGTTGTGTAGCAGGCTGACCAAGATTTCCAGAGGCGCAGTGTGGA 578

QY 1699 TCCACAGACCTTGAAGTTCAAAAGTTTCACAAAGATGAAGATCAGGCTGACCATGTT 1758
    |||
DB 579 TCCACAGACCTTGAAGTTCAAAAGTTTCACAAAGATGAAGATCAGGCTGACCATGTT 638

QY 1759 TGGCAGATATCTATATGAGACAGAGAGTGTGATGCCCCAAGGCAAGGACCTCCAGC 1818
    |||
DB 639 TGGCAGATATCTATATGAGACAGAGAGTGTGATGCCCCAAGGCAAGGACCTCCAGC 698

QY 1819 CAGGCTTCAATTATGCACTTGTGTGCAAAAAGAAAGCTAGTTTAAAGCTGTGCGAG 1878
    |||
DB 699 CAGGCTTCAATTATGCACTTGTGTGCAAAAAGAAAGCTAGTTTAAAGCTGTGCGAG 758

QY 1879 AACCCATCCCAATTAAGAGACCGAGTCTGAAGTCACTATTGATATCTAGTAGAGACT 1938
    |||
DB 759 AACCCATCCCAATTAAGAGACCGAGTCTGAAGTCACTATTGATATCTAGTAGAGACT 818

QY 1939 TGGAGTCAAGCAGTGAAGCTGTGGGGCAAGGGGGGAGTGGGTACTGTAAACCTTAA 1998
    |||
DB 819 TGGAGTCAAGCAGTGAAGCTGTGGGGCAAGGGGGGAGTGGGTACTGTAAACCTTAA 878

QY 1999 AGATGTTAATTCATTCATATAGATATTTATTAAGAACCTAC 2039
    |||
DB 879 AGATGTTAATTCATTCATATAGATATTTATTAAGAACCTAC 919

RESULT 2
US-09-513-999C-395
; Sequence 395, Application US/0951399C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59. US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 395
; LENGTH: 344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 54..344
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 54..119
; OTHER INFORMATION: score 5.9
; FEATURE:
; NAME/KEY: misc_feature
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LOCATION: 197
OTHER INFORMATION: K-g or t
US-09-513-999C-395

Query Match 10.4%; Score 281; DB 4; Length 344;
Best Local Similarity 99.7%; Pred. No. 3.3e-111;
Matches 331; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGTGGCTTCATTTAGAGTGGCTGACATTCAGAGACATATAGCGTGTCCCAACAT 60
DB 13 GGAAGTGGCTTCATTTAGAGTGGCTGACATTCAGAGACATATAGCGTGTCCCAACAT 72
QY 61 GCCTCACCTCATATATATCTTTGAGAGCTCAGAGGTGAGAGCCTCTGACCCCTGA 120
DB 73 GCCTCACCTCATATATCTTTGAGAGCTCAGAGGTGAGAGCCTCTGACCCCTGA 132
QY 121 AAGAGCTGTGCGTTCGTTGGTGGGGCCGTGACCTTCCCTGGAAGTCAAGTAAAGC 180
DB 133 AAGAGCTGTGCGTTCGTTGGTGGGGCCGTGACCTTCCCTGGAAGTCAAGTAAAGC 192
QY 181 AAGTGACTGATTTGCTGACCTTCAACACACCCCTTGTTCACATACAGCCAGAG 240
DB 193 AAGTGACTGATTTGCTGACCTTCAACACACCCCTTGTTCACATACAGCCAGAG 252
QY 241 GGGGCACTATCATAGTACCCAAATGCTAATAGGAGAGATGAGATTCCTCCAGATGAG 300
DB 253 GGGGCACTATCATAGTACCCAAATGCTAATAGGAGAGATGAGATTCCTCCAGATGAG 312
QY 301 GCTACTCCCTGAAAGCTGAGCAAACTGAAGAAG 332
DB 313 GCTACTCCCTGAAAGCTGAGCAAACTGAAGAAG 344

RESULT 3
US-09-513-999C-21312
Sequence 21312, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513, 999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 21312
LENGTH: 435
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-21312

Query Match 6.7%; Score 182; DB 4; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.1e-68;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1857 CTAGAGTTTAAAGCTGTCAGAAACCATCCCAATAAAGAGACCGAGTCTGAAGTCAAT 1916
DB 1 CTAGAGTTTAAAGCTGTCAGAAACCATCCCAATAAAGAGACCGAGTCTGAAGTCAAT 60
QY 1917 TGTAAATCTAGAGTGAAGAGCTTGAGTCAAGCAGTGAAGCTGCTGGGAGCAGCGGGGCA 1976
DB 61 TGTAAATCTAGAGTGAAGAGCTTGAGTCAAGCAGTGAAGCTGCTGGGAGCAGCGGGGCA 120
QY 1977 GTGGGTCTGTGAACCTTTAAAGATGCTTAATTCATTCATATAGATATTTTAAAGAAC 2036
DB 121 GTGGGTCTGTGAACCTTTAAAGATGCTTAATTCATTCATATAGATATTTTAAAGAAC 180
QY 2037 TA 2038

DB 181 TA 182

RESULT 4
US-08-618-100B-3
Sequence 3, Application US/08618100B
Patent No. 6068976

GENERAL INFORMATION:
APPLICANT: Briggs, Michael R.
APPLICANT: Auwerx, Johan
APPLICANT: de Vos, Piet
APPLICANT: Staelen, Bart
APPLICANT: Croston, Glenn E.
APPLICANT: Miller, Stephen G.
TITLE OF INVENTION: MODULATORS OF OB GENE AND
NUMBER OF SEQUENCES: 48
TITLE OF INVENTION: SCREENING METHODS THEREFOR
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,100B
FILING DATE: March 19, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,588
FILING DATE: October 30, 1995
APPLICATION NUMBER: 08/510,584
FILING DATE: August 2, 1995
APPLICATION NUMBER: 08/418,096
FILING DATE: April 5, 1995
APPLICATION NUMBER: 08/408,584
FILING DATE: March 20, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: Sequence between exon 1 and exon 2
Patent No. 6068976
US-08-618-100B-3

Query Match 2.3%; Score 61; DB 3; Length 10684;
Best Local Similarity 100.0%; Pred. No. 9.5e-17;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2107 ATCTGAGTCAGAGATTTCAAGACCCCTGGCCCAAGATGTGAAGAACCCATCTTACTAA 2166
DB 6766 ATCTGAGTCAGAGATTTCAAGACCCCTGGCCCAAGATGTGAAGAACCCATCTTACTAA 6825
QY 2167 A 2167

Db 6826 A 6826

RESULT 5

US-09-506-729-55
; Sequence 55, Application US/09506729
; Patent No. 6365352
; GENERAL INFORMATION:
; APPLICANT: Yerramilli, Subrahmanyam V.
; APPLICANT: Prashar, Yatindra
; APPLICANT: Newberger, Peter
; APPLICANT: Goguen, Jon
; APPLICANT: Weissman, Sherman M.
; TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
; TITLE OF INVENTION: GRANULOCYTIC CELLS
; FILE REFERENCE: 44921-5016-US
; CURRENT APPLICATION NUMBER: US/09/506,729
; EARLIER FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: PCT/US98/17284
; EARLIER FILING DATE: 1998-08-21
; EARLIER APPLICATION NUMBER: 60/056,844
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-506-729-55

Query Match

2.2%; Score 59; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 8, 9e-16;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2616 GCAAAACCTATTGTAGTAAAGTCTTTCTTACTACTTAAATAAAGATATTGTG 2674

DB 15 GCAAAACCTATTGTAGTAAAGTCTTTCTTACTACTTAAATAAAGATATTGTG 73

RESULT 6

US-09-621-976-8541/C
; Sequence 8541, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Ubert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8541
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8541

Query Match

2.2%; Score 59; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 8, 1e-16;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAAGAGTTCAAGACCGCTGGCCAAATGTTAAACCCCATCTTACTTAA 2167

DB 147 CTGAGGTCAAGAGTTCAAGACCGCTGGCCAAATGTTAAACCCCATCTTACTTAA 89

RESULT 7

US-08-531-927B-9
; Sequence 9, Application US/08531927B
; Patent No. 5840491

GENERAL INFORMATION:

; APPLICANT: Kakizuka, Akira
; TITLE OF INVENTION: DNA Sequence Encoding the Machado-Joseph
; Patent No. 5840491
; TITLE OF INVENTION: Disease Gene and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,927B
; FILING DATE: 21-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP H6-251600
; FILING DATE: 21-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: ATH95-01A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-531-927B-9

Query Match

2.2%; Score 59; DB 2; Length 807;
Best Local Similarity 100.0%; Pred. No. 7, 9e-16;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAAGAGTTCAAGACCGCTGGCCAAATGTTAAACCCCATCTTACTTAA 2167

DB 548 CTGAGGTCAAGAGTTCAAGACCGCTGGCCAAATGTTAAACCCCATCTTACTTAA 606

RESULT 8

US-08-531-927B-1
; Sequence 1, Application US/08531927B
; Patent No. 5840491
; GENERAL INFORMATION:
; APPLICANT: Kakizuka, Akira
; TITLE OF INVENTION: DNA Sequence Encoding the Machado-Joseph
; Patent No. 5840491
; TITLE OF INVENTION: Disease Gene and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/531.927B
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP H6-251600
FILING DATE: 21-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: ATH95-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 36..1115
US-08-531-927B-1

Query Match 2.2%; Score 59; DB 2; Length 1776;
Best Local Similarity 100.0%; Pred. No. 7.5e-16;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAAGAGTTCAAGACCAAGCCCTGGCCCAACATGCTGAACCCCATCTCTACTAAA 2167
DB 1535 CTGAGGTCAAGAGTTCAAGACCAAGCCCTGGCCCAACATGCTGAACCCCATCTCTACTAAA 1593

RESULT 9
US-09-041-886-12
Sequence 12, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Shantoz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041.886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

FEATURE:
NAME/KEY: CDS
LOCATION: 36..1116
US-09-041-886-12

Query Match 2.2%; Score 59; DB 3; Length 1776;
Best Local Similarity 100.0%; Pred. No. 7.5e-16;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAAGAGTTCAAGACCAAGCCCTGGCCCAACATGCTGAACCCCATCTCTACTAAA 2167
DB 1535 CTGAGGTCAAGAGTTCAAGACCAAGCCCTGGCCCAACATGCTGAACCCCATCTCTACTAAA 1593

RESULT 10
US-09-526-193A-20/c
Sequence 20, Application US/09526193A
Patent No. 6617122
GENERAL INFORMATION:
APPLICANT: Hayden, Michael R.
APPLICANT: Brooks-Wilson, Angela R.
APPLICANT: Pimstone, Simon N.
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
TITLE OF INVENTION: CHOLESTEROL LEVELS
FILE REFERENCE: 50110/002005
CURRENT APPLICATION NUMBER: US/09/526.193A
CURRENT FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 60/124,702
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: 60/138,048
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/139,600
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: 60/151,977
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 287
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 8981
TYPE: DNA
ORGANISM: Homo sapiens
US-09-526-193A-20

Query Match 2.2%; Score 59; DB 4; Length 8981;
Best Local Similarity 100.0%; Pred. No. 7e-16;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAAGAGTTCAAGACCAAGCCCTGGCCCAACATGCTGAACCCCATCTCTACTAAA 2167
DB 6592 CTGAGGTCAAGAGTTCAAGACCAAGCCCTGGCCCAACATGCTGAACCCCATCTCTACTAAA 6534

RESULT 11
US-09-780-172-18/c
Sequence 18, Application US/09780172
Patent No. 6607916
GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Susan M. Freier
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA EXPRESSION
FILE REFERENCE: RTS-0159
CURRENT APPLICATION NUMBER: US/09/780.172
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 18
LENGTH: 63000
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-780-172-18

Query Match 2.2%; Score 59; DB 4; Length 63000;

Best Local Similarity 100.0%; Pred. No. 6.3e-16;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAAGAGTTCAAGACGAGCTGGCCCAATGTTGAAACCCCATCTCTACTAA 2167
Db 60071 CTGAGGTCAAGAGTTCAAGACGAGCTGGCCCAATGTTGAAACCCCATCTCTACTAA 60013

RESULT 12

US-09-078-294-24
Sequence 24, Application US/09078294
Patent No. 6265211

GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24

LENGTH: 330

TYPE: DNA

ORGANISM: BAC-F2 contig 47 fragment 4
US-09-078-294-24

Query Match

Best Local Similarity 2.1%; Score 58; DB 3; Length 330;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2110 TGAGGTCAAGAGTTCAAGACGAGCTGGCCCAATGTTGAAACCCCATCTCTACTAA 2167
Db 91 TGAGGTCAAGAGTTCAAGACGAGCTGGCCCAATGTTGAAACCCCATCTCTACTAA 148

RESULT 13

US-10-140-002-385/C
Sequence 385, Application US/10140002
Patent No. 6725730

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Inc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geriltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 385

LENGTH: 2749

TYPE: DNA

ORGANISM: Homo Sapien

FEATURE:

NAME/KEY: unsure

LOCATION: 1869, 1887

OTHER INFORMATION: unknown base
US-10-140-002-385

Query Match 2.1%; Score 58; DB 4; Length 2749;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2110 TGAGGTCAAGAGTTCAAGACGAGCTGGCCCAATGTTGAAACCCCATCTCTACTAA 2167
Db 2360 TGAGGTCAAGAGTTCAAGACGAGCTGGCCCAATGTTGAAACCCCATCTCTACTAA 2303

RESULT 14

US-09-078-294-7
Sequence 7, Application US/09078294
Patent No. 6265211

GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7

LENGTH: 11811

TYPE: DNA

ORGANISM: BAC-F2 contig 3
US-09-078-294-7

Query Match

Best Local Similarity 2.1%; Score 58; DB 3; Length 11811;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2110 TGAGGTCAAGAGTTCAAGACGAGCTGGCCCAATGTTGAAACCCCATCTCTACTAA 2167
Db 10756 TGAGGTCAAGAGTTCAAGACGAGCTGGCCCAATGTTGAAACCCCATCTCTACTAA 10813

RESULT 15

US-09-009-217-11
Sequence 11, Application US/09009217
Patent No. 6132729

GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
APPLICANT: Gao, Boning
TITLE OF INVENTION: COMBINED TISSUE FACTOR AND
TITLE OF INVENTION: CHEMOTHERAPEUTIC METHODS AND COMPOSITIONS FOR COAGULATION
TITLE OF INVENTION: AND TUMOR TREATMENT
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,217

FILING DATE: Concurrently Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,427

FILING DATE: 27-MAR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTSD:536
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 13865 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-009-217-11

Query Match 2.1%; Score 58; DB 3; Length 13865;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2110 TGAGTCAGAGATTCAAGACCAAGCTGGCCCAACATGTAAGAAACCCATCTCTACTATAA 2167
DB 8456 TGAGTCAGAGATTCAAGACCAAGCTGGCCCAACATGTAAGAAACCCATCTCTACTATAA 8513

RESULT 16
US-09-009-656-11
Sequence 11, Application US/09009656
Patent No. 6132730
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
APPLICANT: Gao, Boning
TITLE OF INVENTION: COMBINED TISSUE FACTOR AND FACTOR VIIA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR
TITLE OF INVENTION: TREATMENT
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,656
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTSD:537
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 13865 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-009-656-11

Query Match 2.1%; Score 58; DB 3; Length 13865;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2110 TGAGTCAGAGATTCAAGACCAAGCTGGCCCAACATGTAAGAAACCCATCTCTACTATAA 2167
DB 8456 TGAGTCAGAGATTCAAGACCAAGCTGGCCCAACATGTAAGAAACCCATCTCTACTATAA 8513

RESULT 17
US-09-054-272-11
Sequence 11, Application US/09054272
Patent No. 6692909
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Daley, George O.
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Rozen, Steven G.
TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,272
FILING DATE: 01-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI98-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 13865 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
FEATURE:
US-09-054-272-11

Query Match 2.1%; Score 58; DB 4; Length 13865;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2110 TGAGTCAGAGATTCAAGACCAAGCTGGCCCAACATGTAAGAAACCCATCTCTACTATAA 2167

Db 8456 TGAGGTCAGAGGTTCAAGACCGCTGGCCACACATGGTGAAACCCCATCTCTACTTAA 8513

RESULT 18

US-09-759-359A-3/C
; Sequence 3, Application US/09759359A
; Patent No. 6492153
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: CL001043
; CURRENT APPLICATION NUMBER: US/09/759,359A
; CURRENT FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 90541
; TYPE: DNA
; ORGANISM: Human
US-09-759-359A-3

Query Match 2.1%; Score 58; DB 4; Length 90541;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2110 TGAGGTCAGAGGTTCAAGACCGCTGGCCACACATGGTGAAACCCCATCTCTACTTAA 2167
Db 5701 TGAGGTCAGAGGTTCAAGACCGCTGGCCACACATGGTGAAACCCCATCTCTACTTAA 5644

RESULT 19

US-10-207-973-3/C
; Sequence 3, Application US/10207973
; Patent No. 6753175
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: CL001043
; CURRENT APPLICATION NUMBER: US/10/207,973
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 90541
; TYPE: DNA
; ORGANISM: Human
US-10-207-973-3

Query Match 2.1%; Score 58; DB 4; Length 90541;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2110 TGAGGTCAGAGGTTCAAGACCGCTGGCCACACATGGTGAAACCCCATCTCTACTTAA 2167
Db 5701 TGAGGTCAGAGGTTCAAGACCGCTGGCCACACATGGTGAAACCCCATCTCTACTTAA 5644

RESULT 20

US-09-754-250-3/C
; Sequence 3, Application US/09754250
; Patent No. 6376225
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063
; CURRENT APPLICATION NUMBER: US/09/754,250
; CURRENT FILING DATE: 2001-01-05

; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 111282
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(11282)
; OTHER INFORMATION: n = A,T,C or G
US-09-754-250-3

Query Match 2.1%; Score 58; DB 3; Length 111282;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2110 TGAGGTCAGAGGTTCAAGACCGCTGGCCACACATGGTGAAACCCCATCTCTACTTAA 2167
Db 14711 TGAGGTCAGAGGTTCAAGACCGCTGGCCACACATGGTGAAACCCCATCTCTACTTAA 14654

RESULT 21

US-08-599-252-94
; Sequence 94, Application US/08599252
; Patent No. 5705343
; GENERAL INFORMATION:
; APPLICANT: DRAYNA, DENNIS T.
; APPLICANT: FEDER, JOHN N.
; APPLICANT: GRIKKE, ANDREAS
; APPLICANT: KIMMEL, BRUCE E.
; APPLICANT: THOMAS, WINSTON J.
; APPLICANT: WOLFF, ROGER K.
; TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
; TITLE OF INVENTION: HEMOCHROMATOSIS
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,252
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 9053-0001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-599-252-94

Query Match 2.1%; Score 57; DB 1; Length 688;
Best Local Similarity 100.0%; Pred. No. 5.7e-15;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2109 TGAGGTCAGAGGTTCAAGACCGCTGGCCACACATGGTGAAACCCCATCTCTACTTAA 2165

Db 7 CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

RESULT 22
PCT-US96-06352-94

Sequence 94, Application PC/TUS9606352

GENERAL INFORMATION:

APPLICANT: DRAVNA, DENNIS T.

APPLICANT: FEDER, JOHN N.

APPLICANT: GINKEL, ANDREAS

APPLICANT: KIMMEL, BRUCE E.

APPLICANT: THOMAS, WINSTON J.

APPLICANT: WOLFF, ROGER K.

TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY

TITLE OF INVENTION: HEMOCHROMATOSIS

NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Ave. N.W., Suite 5500

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/06352

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/599,252

FILING DATE: 09-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 9053-0001.21

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 94:

SEQUENCE CHARACTERISTICS:

LENGTH: 688 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

PCT-US96-06352-94

Query Match

Best Local Similarity 100.0%; Score 57; DB 5; Length 688;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

2109 CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 2165

CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Ave. N.W., Suite 5500

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/06583

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/599,252

FILING DATE: 09-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 9053-0001.21

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 94:

SEQUENCE CHARACTERISTICS:

LENGTH: 688 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

PCT-US96-06583-94

Query Match

Best Local Similarity 100.0%; Score 57; DB 5; Length 688;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

2109 CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 2165

CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

CTGAGGTCAAGAGTTCAAGACCAAGCTGCGCCACATGCTGAACCCTCTCTACTA 63

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 GAGGTCAAGAGTTCAAGACCAAGCCTGGCCAAACATGTTGAAACCCCATCTTACTTAA 2167
|||||
DB 35735 GAGGTCAAGAGTTCAAGACCAAGCCTGGCCAAACATGTTGAAACCCCATCTTACTTAA 35791

RESULT 25
US-09-543-771-11
; Sequence 11, Application US/09543771
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: John P. Carulli et al.
; TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/543,771
; EARLIER FILING DATE: 2000-04-05
; EARLIER APPLICATION NUMBER: US 09/229,319
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 60/071,449
; EARLIER FILING DATE: 1998-01-13
; EARLIER APPLICATION NUMBER: US 60/105,511
; EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 62
; SEQ ID NO 11
; LENGTH: 66933
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-543-771-11

Query Match 2.1%; Score 57; DB 4; Length 66933;
Best Local Similarity 100.0%; Pred. No. 4.5e-15;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 GAGGTCAAGAGTTCAAGACCAAGCCTGGCCAAACATGTTGAAACCCCATCTTACTTAA 2167
|||||
DB 35735 GAGGTCAAGAGTTCAAGACCAAGCCTGGCCAAACATGTTGAAACCCCATCTTACTTAA 35791

RESULT 26
US-09-544-398B-9
; Sequence 9, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark U.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 72049
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (8356),(8385),(38585)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
US-09-544-398B-9

Query Match 2.1%; Score 57; DB 4; Length 72049;
Best Local Similarity 100.0%; Pred. No. 4.5e-15;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 GAGTCAGAGTTCAAGACCAAGCCTGGCCAAACATGTTGAAACCCCATCTTACTTAA 2167
|||||
DB 39324 GAGTCAGAGTTCAAGACCAAGCCTGGCCAAACATGTTGAAACCCCATCTTACTTAA 39380

RESULT 27
US-09-543-771-9
; Sequence 9, Application US/09543771
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: John P. Carulli et al.
; TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/543,771
; EARLIER FILING DATE: 2000-04-05
; EARLIER APPLICATION NUMBER: US 09/229,319
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 60/071,449
; EARLIER FILING DATE: 1998-01-13
; EARLIER APPLICATION NUMBER: US 60/105,511
; EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 62
; SEQ ID NO 9
; LENGTH: 72049
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (8356),(8385),(38585)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
US-09-543-771-9

Query Match 2.1%; Score 57; DB 4; Length 72049;
Best Local Similarity 100.0%; Pred. No. 4.5e-15;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 GAGTCAGAGTTCAAGACCAAGCCTGGCCAAACATGTTGAAACCCCATCTTACTTAA 2167
|||||
DB 39324 GAGTCAGAGTTCAAGACCAAGCCTGGCCAAACATGTTGAAACCCCATCTTACTTAA 39380

RESULT 28
US-09-513-999C-35299/C
; Sequence 35299, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Meline Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2,REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 35299
; LENGTH: 153
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-35299

Query Match 2.1%; Score 56; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.7e-14;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 GAGTCAGAGTTCAAGACCAAGCCTGGCCAAACATGTTGAAACCCCATCTTACTTAA 2166
|||||
DB 56 GAGTCAGAGTTCAAGACCAAGCCTGGCCAAACATGTTGAAACCCCATCTTACTTAA 1

RESULT 29

US-09-534-638-3
; Sequence 3, Application US/09534638
; Patent No. 6320038
; GENERAL INFORMATION:
; APPLICANT: Panula, Pereti A.J.
; APPLICANT: Brandt, Annika
; APPLICANT: Meesterlund, Johanna
; TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use thereof
; TITLE OF INVENTION: For therapy and diagnosis
; FILE REFERENCE: 2530-104
; CURRENT APPLICATION NUMBER: US/09/534,638
; CURRENT FILING DATE: 2000-03-27
; EARLIER APPLICATION NUMBER: 09/365755
; EARLIER FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-534-638-3

Query Match 2.0%; Score 55; DB 3; Length 2480;
Best Local Similarity 100.0%; Pred. No. 3,9e-14;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2110 TGAGGTGAGAGTTCAAGACCAGCTGGCCCAACATGTGTGAACCCCATCTTACT 2164
DB 216 TGAGGTGAGAGTTCAAGACCAGCTGGCCCAACATGTGTGAACCCCATCTTACT 270

RESULT 30

US-09-621-976-691
; Sequence 691, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patentln.pm
; SEQ ID NO 691
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 263..472
US-09-621-976-691

Query Match 2.0%; Score 54; DB 4; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2110 TGAGGTGAGAGTTCAAGACCAGCTGGCCCAACATGTGTGAACCCCATCTTACT 2163
DB 333 TGAGGTGAGAGTTCAAGACCAGCTGGCCCAACATGTGTGAACCCCATCTTACT 386

RESULT 31

US-09-435-739-42
; Sequence 42, Application US/09435739
; Patent No. 6664105
; GENERAL INFORMATION:
; APPLICANT: Pecker, Irit
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena

; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS

; FILE REFERENCE: 00/20454
; CURRENT APPLICATION NUMBER: US/09/435,739
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 42
; LENGTH: 44848
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-435-739-42

Query Match 2.0%; Score 54; DB 4; Length 44848;
Best Local Similarity 100.0%; Pred. No. 9e-14;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTGAGAGTTCAAGACCAGCTGGCCCAACATGTGTGAACCCCATCTCTA 2162
DB 12111 CTGAGGTGAGAGTTCAAGACCAGCTGGCCCAACATGTGTGAACCCCATCTCTA 12164

RESULT 32

US-09-988-113-42
; Sequence 42, Application US/09988113
; Patent No. 6790658
; GENERAL INFORMATION:
; APPLICANT: Pecker, Irit
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 01/22781
; CURRENT APPLICATION NUMBER: US/09/988,113
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 09/776,874
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US09/258,892
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 42
; LENGTH: 44848
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-988-113-42

Query Match 2.0%; Score 54; DB 4; Length 44848;
Best Local Similarity 100.0%; Pred. No. 9e-14;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTGAGAGTTCAAGACCAGCTGGCCCAACATGTGTGAACCCCATCTCTA 2162
DB 12111 CTGAGGTGAGAGTTCAAGACCAGCTGGCCCAACATGTGTGAACCCCATCTCTA 12164

RESULT 33

US-09-751-389-3/c
; Sequence 3, Application US/09751389
; Patent No. 6630334
; GENERAL INFORMATION:
; APPLICANT: GUGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001067
; CURRENT APPLICATION NUMBER: US/09/751,389

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/ CURRENT FILING DATE: 2001-01-02
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 786431
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(786431)
/ OTHER INFORMATION: n = A,T,C or G
US-09-751-389-3

Query Match          2.0%; Score 54; DB 4; Length 786431;
Best Local Similarity 100.0%; Pred. No. 7.8e-14;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2050 GGCATGCTGCTACACCTGTATCCAGCAGCTTTGGAGAGCCCAAGTGGTGG
DB      251148 GGCATGCTGCTACACCTGTATCCAGCAGCTTTGGAGAGCCCAAGTGGTGG 251095

RESULT 34
US-08-611-587-1
/ Sequence 1, Application US/08611587
/ Patent No. 6150091
/ GENERAL INFORMATION:
/ APPLICANT: PANDOLFO, MASSIMO
/ APPLICANT: MONTERMINI, LAURA
/ APPLICANT: MOLITO, MARIA D.
/ APPLICANT: Koenig, Michael
/ APPLICANT: Campuzano, Victoria
/ APPLICANT: Cossee, Mireille
/ TITLE OF INVENTION: Direct Diagnosis of Friedreich Ataxia
/ NUMBER OF SEQUENCES: 33
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fulbright & Jaworski L.L.P. Patent Dept.
/ STREET: 1301 McKinney, Suite 5100
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: U.S.
/ ZIP: 77010
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/611,587
/ FILING DATE: 03-MAR-1996
/ CLASSIFICATION: 436
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Brashears-Macatee, Sarah J.
/ REGISTRATION NUMBER: 38,087
/ REFERENCE/DOCKET NUMBER: D-5901
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 713-651-5620
/ TELEFAX: 713-651-5246
/ TELEX: 76-2829
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8353 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapien
/ POSITION IN GENOME:
/ CHROMOSOME/SEGMENT: 9q13
/ UNITS: bp
```

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US-08-611-587-1

Query Match          2.0%; Score 53; DB 3; Length 8353;
Best Local Similarity 100.0%; Pred. No. 2.6e-13;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2115 TCAGAGTTCAAGACCGCTGGCCCAACATGTTGAACCCCATCTCTATAA 2167
DB      5792 TCAGAGTTCAAGACCGCTGGCCCAACATGTTGAACCCCATCTCTATAA 5844

RESULT 35
US-09-818-512-3
/ Sequence 3, Application US/09818512
/ Patent No. 6537780
/ GENERAL INFORMATION:
/ APPLICANT: BRASLEY, Ellen et al.
/ TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
/ FILE REFERENCE: CL001192
/ CURRENT APPLICATION NUMBER: US/09/818,512
/ CURRENT FILING DATE: 2001-03-28
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 116592
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(116592)
/ OTHER INFORMATION: n = A,T,C or G
US-09-818-512-3

Query Match          2.0%; Score 53; DB 4; Length 116592;
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2109 CTGAGTCAAGAGTTCAAGACCGCTGGCCCAACATGTTGAACCCCATCTCT 2161
DB      24563 CTGAGTCAAGAGTTCAAGACCGCTGGCCCAACATGTTGAACCCCATCTCT 24615

RESULT 36
US-09-671-317-485
/ Sequence 485, Application US/09671317
/ Patent No. 6528260
/ GENERAL INFORMATION:
/ APPLICANT: Blumenfeld, Marta
/ APPLICANT: Chumakov, Ilya
/ APPLICANT: Bougueleret, Lydie
/ APPLICANT: Cohen, Annick
/ TITLE OF INVENTION: BIOMIMETIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
/ FILE REFERENCE: 62.US3.CIP
/ CURRENT APPLICATION NUMBER: US/09/671,317
/ CURRENT FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: US 09/536,178
/ PRIOR FILING DATE: 2000-03-23
/ PRIOR APPLICATION NUMBER: PCT/IB00/00403
/ PRIOR FILING DATE: 2000-03-24
/ PRIOR APPLICATION NUMBER: US 60/126,269
/ PRIOR FILING DATE: 1999-03-25
/ PRIOR APPLICATION NUMBER: US 60/131,961
/ PRIOR FILING DATE: 1999-04-30
/ NUMBER OF SEQ ID NOS: 977
/ SOFTWARE: Patent.pm
/ SEQ ID NO 485
/ LENGTH: 49312
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
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LOCATION: 5466..7466
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
LOCATION: 7467..7725
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 20256..20355
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 36905..36975
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 45167..45248
OTHER INFORMATION: exon 4
NAME/KEY: exon
LOCATION: 45728..45965
OTHER INFORMATION: exon 5
NAME/KEY: misc feature
LOCATION: 45966..49312
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 7564
OTHER INFORMATION: 10-286-289 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 7619
OTHER INFORMATION: 10-286-345 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 7649
OTHER INFORMATION: 10-286-375 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 17258
OTHER INFORMATION: 12-425-57 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 21590
OTHER INFORMATION: 12-421-135 : insertion of T
NAME/KEY: allele
LOCATION: 21595
OTHER INFORMATION: 12-421-140 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 36971
OTHER INFORMATION: 10-523-232 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 45214
OTHER INFORMATION: 10-289-201 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 45741
OTHER INFORMATION: 10-290-37 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 46029
OTHER INFORMATION: 10-290-326 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 46032
OTHER INFORMATION: 10-290-328 : deletion of G
NAME/KEY: primer bind
LOCATION: 7276..7294
OTHER INFORMATION: 10-286.pu
NAME/KEY: primer bind
LOCATION: 7676..7694
OTHER INFORMATION: 10-286.pu
NAME/KEY: primer bind
LOCATION: 16839..16856
OTHER INFORMATION: 12-425.tp
NAME/KEY: primer bind
LOCATION: 17297..17314
OTHER INFORMATION: 12-425.pu complement
NAME/KEY: primer bind
LOCATION: 21456..21474
OTHER INFORMATION: 12-421.pu
NAME/KEY: primer bind
LOCATION: 21886..21906
OTHER INFORMATION: 12-421.tp complement
NAME/KEY: primer bind
LOCATION: 36740..36758

OTHER INFORMATION: 10-523.pu
NAME/KEY: primer bind
LOCATION: 36997..37015
OTHER INFORMATION: 10-523.tp complement
NAME/KEY: primer bind
LOCATION: 45020..45037
OTHER INFORMATION: 10-289.pu
NAME/KEY: primer bind
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LOCATION: 7545..7563
OTHER INFORMATION: 10-286-289.mis
NAME/KEY: primer bind
LOCATION: 7565..7583
OTHER INFORMATION: 10-286-289.mis complement
NAME/KEY: primer bind
LOCATION: 7600..7618
OTHER INFORMATION: 10-286-345.mis
NAME/KEY: primer bind
LOCATION: 7620..7638
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NAME/KEY: primer bind
LOCATION: 7630..7648
OTHER INFORMATION: 10-286-375.mis
NAME/KEY: primer bind
LOCATION: 7650..7668
OTHER INFORMATION: 10-286-375.mis complement
NAME/KEY: primer bind
LOCATION: 17239..17257
OTHER INFORMATION: 12-425-57.mis
NAME/KEY: primer bind
LOCATION: 17259..17277
OTHER INFORMATION: 12-425-57.mis complement
NAME/KEY: primer bind
LOCATION: 21576..21594
OTHER INFORMATION: 12-421-140.mis
NAME/KEY: primer bind
LOCATION: 21596..21614
OTHER INFORMATION: 12-421-140.mis complement
NAME/KEY: primer bind
LOCATION: 36952..36970
OTHER INFORMATION: 10-523-232.mis
NAME/KEY: primer bind
LOCATION: 36972..36990
OTHER INFORMATION: 10-523-232.mis complement
NAME/KEY: primer bind
LOCATION: 45195..45213
OTHER INFORMATION: 10-289-201.mis
NAME/KEY: primer bind
LOCATION: 45215..45233
OTHER INFORMATION: 10-289-201.mis complement
NAME/KEY: primer bind
LOCATION: 45722..45740
OTHER INFORMATION: 10-290-37.mis
NAME/KEY: primer bind
LOCATION: 45742..45760
OTHER INFORMATION: 10-290-37.mis complement
NAME/KEY: primer bind
LOCATION: 46010..46028
OTHER INFORMATION: 10-290-326.mis
NAME/KEY: primer bind
LOCATION: 46030..46048
OTHER INFORMATION: 10-290-326.mis complement
NAME/KEY: misc_binding
LOCATION: 7552..7576
OTHER INFORMATION: 10-286-289.probe

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/ NAME/KEY: misc_binding
/ LOCATION: 7607..7631
/ OTHER INFORMATION: 10-286-345.probe
/ NAME/KEY: misc_binding
/ LOCATION: 7637..7661
/ OTHER INFORMATION: 10-286-375.probe
/ NAME/KEY: misc_binding
/ LOCATION: 17246..17270
/ OTHER INFORMATION: 12-425-57.probe
/ NAME/KEY: misc_binding
/ LOCATION: 21583..21607
/ OTHER INFORMATION: 12-421-140.probe
/ NAME/KEY: misc_binding
/ LOCATION: 36959..36983
/ OTHER INFORMATION: 10-523-232.probe
/ NAME/KEY: misc_binding
/ LOCATION: 45202..45226
/ OTHER INFORMATION: 10-289-201.probe
/ NAME/KEY: misc_binding
/ LOCATION: 45729..45753
/ OTHER INFORMATION: 10-290-37.probe
/ NAME/KEY: misc_binding
/ LOCATION: 46017..46041
/ OTHER INFORMATION: 10-290-326.probe
/ US-09-671-317-485
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Query Match 1.9%; Score 52; DB 4; Length 49312;
Best Local Similarity 100.0%; Pred. No. 6.5e-13;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 2110 TCAGAGTTCAAGACCGCTGGCCCAACATGTGTAACCCCATCTCT 2161
DB 16276 TCAGGTCAAGAGATTCAAGACCGCTGGCCCAACATGTGTAACCCCATCTCT 16327
```

```
RESULT 37
US-09-497-855A-32
/ Sequence 32, Application US/09497855A
/ Patent No. 6605432
/ GENERAL INFORMATION:
/ APPLICANT: Huang, Tim
/ TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
/ FILE REFERENCE: UMO1523
/ CURRENT APPLICATION NUMBER: US/09/497,855A
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: 60/120,592
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: 60/118,760
/ PRIOR FILING DATE: 1999-02-05
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: Patent version 3.0
/ SEQ ID NO 32
/ LENGTH: 118067
/ TYPE: DNA
/ ORGANISM: Homo sapiens;
/ US-09-497-855A-32
```

```
Query Match 1.9%; Score 51; DB 4; Length 118067;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2116 CAGAGTTCAAGACCGCTGGCCCAACATGTGTAACCCCATCTCTACTAA 2166
DB 14295 CAGGAGTTCAAGACCGCTGGCCCAACATGTGTAACCCCATCTCTACTAA 14345
```

```
RESULT 38
US-09-621-976-12888
/ Sequence 12888, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S.
```

```
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 12888
/ LENGTH: 297
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-621-976-12888
```

```
Query Match 1.8%; Score 50; DB 4; Length 297;
Best Local Similarity 100.0%; Pred. No. 6.1e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 2115 TCAGAGTTCAAGACCGCTGGCCCAACATGTGTAACCCCATCTCTACT 2164
DB 89 TCAGAGTTCAAGACCGCTGGCCCAACATGTGTAACCCCATCTCTACT 138
```

```
RESULT 39
US-09-621-976-12887
/ Sequence 12887, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 12887
/ LENGTH: 307
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 305
/ OTHER INFORMATION: n=a, g, c or t
/ US-09-621-976-12887
```

```
Query Match 1.8%; Score 50; DB 4; Length 307;
Best Local Similarity 100.0%; Pred. No. 6.1e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 2115 TCAGAGTTCAAGACCGCTGGCCCAACATGTGTAACCCCATCTCTACT 2164
DB 89 TCAGAGTTCAAGACCGCTGGCCCAACATGTGTAACCCCATCTCTACT 138
```

```
RESULT 40
US-09-621-976-9714/C
/ Sequence 9714, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 9714
/ LENGTH: 369
/ TYPE: DNA
/ ORGANISM: Homo sapiens
```



```
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ PATENT NO. 6783961
/ FILE REFERENCE: 59, US2, REG
/ CURRENT APPLICATION NUMBER: US/09/513,999C
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/122,487
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36681
/ SOFTWARE: Patent.pm
/ SEQ ID NO 30096
/ LENGTH: 191
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-513-999C-30096

Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2055 GGTGGCTCACACCTGTATCCAGACATTGGAGGCCAAGTGGTGG 2103
DB 59 GGTGGCTCACACCTGTATCCAGACATTGGAGGCCAAGTGGTGG 107

RESULT 46
US-09-513-999C-29901/C
/ Sequence 29901, Application US/09513999C
/ Patent No. 6783961
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Duclert, A.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ Patent No. 6783961
/ FILE REFERENCE: 59, US2, REG
/ CURRENT APPLICATION NUMBER: US/09/513,999C
/ CURRENT FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/122,487
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36681
/ SOFTWARE: Patent.pm
/ SEQ ID NO 29901
/ LENGTH: 256
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-513-999C-29901

Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAAGAGTTCAGGCGGCGCAACATGTAAGAACCCCAT 2157
DB 232 CTGAGGTCAAGAGTTCAGGCGGCGCAACATGTAAGAACCCCAT 184

RESULT 47
US-09-621-976-1354/C
/ Sequence 1354, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET, 054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 1354
/ LENGTH: 511
```

```
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 183..398
/ NAME/KEY: sig_peptide
/ LOCATION: 183..251
/ OTHER INFORMATION: Von Heijne matrix
/ OTHER INFORMATION: score 11.1000003814697
/ OTHER INFORMATION: seq LFLLLFLRLSLT/LS
US-09-621-976-1354

Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAAGAGTTCAGGCGGCGCAACATGTAAGAACCCCAT 2157
DB 452 CTGAGGTCAAGAGTTCAGGCGGCGCAACATGTAAGAACCCCAT 404

RESULT 48
US-08-480-784-20/C
/ Sequence 20, Application US/08480784
/ Patent No. 5693473
/ GENERAL INFORMATION:
/ APPLICANT: Skolnick, Mark H.
/ APPLICANT: Goldgar, David E.
/ APPLICANT: Miki, Yoshio
/ APPLICANT: Swenson, Jeff
/ APPLICANT: Kamb, Alexander
/ APPLICANT: Harshman, Keith D.
/ APPLICANT: Shattuck-Eidens, Donna M.
/ APPLICANT: Tavtigian, Sean V.
/ APPLICANT: Wiseman, Roger W.
/ APPLICANT: Futreal, P. Andrew
/ TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
/ NUMBER OF SEQUENCES: 85
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
/ STREET: 1201 New York Avenue, N.W., Suite 1000
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/480,784
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/409,305
/ FILING DATE: 24-MAR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/348,824
/ FILING DATE: 29-NOV-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/308,104
/ FILING DATE: 16-SEP-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/300,266
/ FILING DATE: 02-SEP-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/289,221
/ FILING DATE: 12-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Immen, Jeffrey L.
/ REGISTRATION NUMBER: 28,957
```

REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-480-784-20

Query Match 1.8%; Score 49; DB 1; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2119 GAGTTCAGACCGCCTGGCCACATGTGAAACCCCATCTTACTAA 2167
DB 5670 GAGTTCAGACCGCCTGGCCACATGTGAAACCCCATCTTACTAA 5622

RESULT 49
US-08-483-553-20/c
Sequence 20, Application US/08483553
Patent No. 5709999
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Hareham, Keith D.
APPLICANT: Shatluck-Eldens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSES: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,553
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-483-553-20

Query Match 1.8%; Score 49; DB 1; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2119 GAGTTCAGACCGCCTGGCCACATGTGAAACCCCATCTTACTAA 2167
DB 5670 GAGTTCAGACCGCCTGGCCACATGTGAAACCCCATCTTACTAA 5622

RESULT 50
US-08-487-002-20/c
Sequence 20, Application US/08487002
Patent No. 5710001
GENERAL INFORMATION:
APPLICANT: Shatluck-Eldens, Donna M.
APPLICANT: Simard, Jacques
APPLICANT: Emi, Mitsuru
APPLICANT: Nakamura, Yusuke
APPLICANT: Durocher, Francine
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSES: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,002
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ. ID NO.: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-487-002-20

Query Match 1.8%; Score 49; DB 1; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2119 GAGTCAAGACCGAGCTGGCCAAACATGGTGAACCCCATCTACTAA 2167
DB 5670 GAGTCAAGACCGAGCTGGCCAAACATGGTGAACCCCATCTACTAA 5622

RESULT 51

US-08-483-554B-20/c
Sequence 20, Application US/08483554B

GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,554B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104

FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ. ID NO.: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-483-554B-20

Query Match 1.8%; Score 49; DB 1; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2119 GAGTCAAGACCGAGCTGGCCAAACATGGTGAACCCCATCTACTAA 2167
DB 5670 GAGTCAAGACCGAGCTGGCCAAACATGGTGAACCCCATCTACTAA 5622

RESULT 52

US-08-488-011B-20/c
Sequence 20, Application US/08488011B

GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,011B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347-09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Homo sapiens
US-08-488-0118-20

Query Match 1.8%; Score 49; DB 1; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2119 GAGTTCAAGACGAGCCTGGCCCAACATGTGTGAACCCCATCTCTACTAA 2167
Db 5670 GAGTTCAAGACGAGCCTGGCCCAACATGTGTGAACCCCATCTCTACTAA 5622

RESULT 53
US-08-850-727-20/c
Sequence 20, Application US/08850727
Patent No. 6162897
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Hershman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,727

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,554
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Homo sapiens
US-08-850-727-20

Query Match 1.8%; Score 49; DB 3; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2119 GAGTTCAAGACGAGCCTGGCCCAACATGTGTGAACCCCATCTCTACTAA 2167
Db 5670 GAGTTCAAGACGAGCCTGGCCCAACATGTGTGAACCCCATCTCTACTAA 5622

RESULT 54
PCT-US95-10202-20/c
Sequence 20, Application PC/TUS9510202
GENERAL INFORMATION:
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Simard, Jacques
APPLICANT: Emi, Mitsuhiro
APPLICANT: Nakamura, Yusuke
APPLICANT: Durocher, Francine
TITLE OF INVENTION: In Vivo Mutations and Polymorphisms
TITLE OF INVENTION: in the 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10202

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08-308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PCT-US95-10202-20

Query Match 1.8%; Score 49; DB 5; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2119 GAGTCAAGACGAGCCTGGCCAAACATGGTGAACCCCATCTACTATAA 2167
DB 5670 GAGTCAAGACGAGCCTGGCCAAACATGGTGAACCCCATCTACTATAA 5622

RESULT 55
PCT-US95-10203-20/c
Sequence 20, Application PC/TUS9510203
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Bidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10203
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08-308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6769 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PCT-US95-10203-20

Query Match 1.8%; Score 49; DB 5; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2119 GAGTCAAGACGAGCCTGGCCAAACATGGTGAACCCCATCTACTATAA 2167
DB 5670 GAGTCAAGACGAGCCTGGCCAAACATGGTGAACCCCATCTACTATAA 5622

RESULT 56
PCT-US95-10220-20/c
Sequence 20, Application PC/TUS9510220
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Bidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: Method for Diagnosing a
TITLE OF INVENTION: Predisposition for Breast and Ovarian Cancer
NUMBER OF SEQUENCES: 85

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
;; STREET: 1201 New York Avenue, N.W., Suite 1000
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/10220
;; FILING DATE:
;; CLASSIFICATION:
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US
;; FILING DATE: 07-JUN-1995
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/409,305
;; FILING DATE: 24-MAR-1995
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/348,824
;; FILING DATE: 29-NOV-1994
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08-308,104
;; FILING DATE: 16-SEP-1994
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/300,266
;; FILING DATE: 02-SEP-1994
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/289,221
;; FILING DATE: 12-AUG-1994
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ihnen, Jeffrey L.
;; REGISTRATION NUMBER: 28,957
;; REFERENCE/DOCKET NUMBER: 24884-109347.
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-962-4810
;;
;; TELEFAX: 202-962-8300
;;
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6769 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; PCT-US95-10220-20
;;
Query Match 1.8%; Score 49; DB 5; Length 6769;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;;
QY 2119 GAGTTCAAGACACGCTGGCCACATGATGTAACCCCATCTCTACTAA 2167
Db 5670 GAGTTCAAGACACGCTGGCCACATGATGTAACCCCATCTCTACTAA 5622
;;
RESULT 57
US-07-914-281-5/c
; Sequence 5, Application US/07914281
; Patent No. 5324663
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU

;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; STREET: 1755 Jefferson Davis Highway, Fourth Floor
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: U.S.A.
;; ZIP: 22202
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/914,281
;; FILING DATE: 19920720
;; CLASSIFICATION: 530
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lavalleye, Jean-Paul M. P.
;; REGISTRATION NUMBER: 31,451
;; REFERENCE/DOCKET NUMBER: 2363-060-55
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703)521-4500
;; TELEFAX: (703)486-2347
;; TELEX: 248855 OPAT UR
;;
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8174 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: DNA (genomic)
;; ANTI-SENSE: NO
;; US-07-914-281-5
;;
Query Match 1.8%; Score 49; DB 1; Length 8174;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;;
QY 2055 GGTGGCTCACACCTGTATCCAGCACTTTGGAGGCCAAGTGGGTGG 2103
Db 4287 GGTGGCTCACACCTGTATCCAGCACTTTGGAGGCCAAGTGGGTGG 4239
;;
RESULT 58
US-08-393-246-5/c
; Sequence 5, Application US/08393246
; Patent No. 5595900
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; STREET: 1755 Jefferson Davis Highway, Fourth Floor
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: U.S.A.
;; ZIP: 22202
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/393,246
;; FILING DATE:
;; CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8174 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-393-246-5

Query Match 1.8%; Score 49; DB 1; Length 8174;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2055 GGTCGCTCACACCTGTATCCAGACCTTTGGAGGCCAAGTGGGTGG 2103
DB 4287 GGTGGCTCACACCTGTATCCAGACCTTTGGAGGCCAAGTGGGTGG 4239

RESULT 59

US-08-525-058A-5/C
Sequence 5, Application US/08525058A
Patent No. 5770420
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P. C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
City: Arlington
State: Virginia
Country: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,058A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8174 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-525-058A-5

Query Match 1.8%; Score 49; DB 1; Length 8174;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2055 GGTCGCTCACACCTGTATCCAGACCTTTGGAGGCCAAGTGGGTGG 2103
DB 4287 GGTGGCTCACACCTGTATCCAGACCTTTGGAGGCCAAGTGGGTGG 4239

RESULT 60

US-08-696-731-5/C
Sequence 5, Application US/08696731
Patent No. 595347
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: P. C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
City: Arlington
State: Virginia
Country: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,731
FILING DATE: 14-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/393,246
FILING DATE:
APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8174 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-696-731-5

Query Match 1.8%; Score 49; DB 2; Length 8174;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2055 GGTCGCTCACACCTGTATCCAGACCTTTGGAGGCCAAGTGGGTGG 2103
DB 4287 GGTGGCTCACACCTGTATCCAGACCTTTGGAGGCCAAGTGGGTGG 4239

```

RESULT 61
US-09-042-531-5/c
; Sequence 5, Application US/09042531
; Patent No. 6268193
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042.531
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/393.246
; FILING DATE:
; APPLICATION NUMBER: US 08/220.433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914.281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8174 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-09-042-531-5

Query Match 1.8%; Score 49; DB 3; Length 8174;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2055 GGAGGCTCACACCTGTATCCAGCACTTTGGAGGCCAAGTGGTGG 2103
Db 4287 GGAGGCTCACACCTGTATCCAGCACTTTGGAGGCCAAGTGGTGG 4239

RESULT 62
PCT-US91-00899-3/c
; Sequence 3, Application PC/TUS9100899
; GENERAL INFORMATION:
; APPLICANT: Lowe, John B.
; TITLE OF INVENTION: Method and Products For the Synthesis of
; OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS, GLYCOLIPIDS,
; TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned
; TITLE OF INVENTION: Genetic Sequences That Determine These Structur

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; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00899
; FILING DATE: 19910214
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye Ph.D., Jean-Paul
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-021-55 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-5940
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8174 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Blood
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 4686..5780
; OTHER INFORMATION: /label= mat_peptide
; PCT-US91-00899-3

Query Match 1.8%; Score 49; DB 5; Length 8174;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2055 GGAGGCTCACACCTGTATCCAGCACTTTGGAGGCCAAGTGGTGG 2103
Db 4287 GGAGGCTCACACCTGTATCCAGCACTTTGGAGGCCAAGTGGTGG 4239

RESULT 63
US-09-345-882-1/c
; Sequence 1, Application US/09345882
; Patent No. 6399373
; GENERAL INFORMATION:
; APPLICANT: Bouguetieret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
; FILE REFERENCE: GENSET.031A
; CURRENT APPLICATION NUMBER: US/09/345.882
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091.315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111.909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 162450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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NAME/KEY: allele
LOCATION: 72794
OTHER INFORMATION: 5-124-273 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 90842
OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 93714
OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
FEATURE:
NAME/KEY: allele
LOCATION: 97122
OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
FEATURE:
NAME/KEY: allele
LOCATION: 99098
OTHER INFORMATION: 5-130-257 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 99117
OTHER INFORMATION: 5-130-276 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 103806
OTHER INFORMATION: 5-131-395 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
FEATURE:
NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 108471
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134362
OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE:
NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele

LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140

OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:

Query Match 1.8%; Score 49; DB 3; Length 162450;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAGAGTTCAAGACCAAGCCCTGGCCCAACATGTTGAACCCCA 2157
DB 153776 CTGAGGTCAGAGTTCAAGACCAAGCCCTGGCCCAACATGTTGAACCCCA 153728

RESULT 64
US-09-513-999C-20281
Sequence 20281, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J. B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J. Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513, 999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 20281
LENGTH: 141
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-20281

Query Match 1.8%; Score 48; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2109 CTGAGGTCAGAGTTCAAGACCAAGCCCTGGCCCAACATGTTGAACCCCA 2156
|||||

DB 92 CTGAGGTCAGAGTTCAAGACCAAGCCCTGGCCCAACATGTTGAACCCCA 139

RESULT 65
US-08-916-901-6
Sequence 6, Application US/08916901
Patent No. 5892012
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Puri
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916, 901
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-916-901-6

Query Match 1.8%; Score 48; DB 2; Length 2713;
Best Local Similarity 100.0%; Pred. No. 3.9e-11;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAGAGTTCAAGACCAAGCCCTGGCCCAACATGTTGAACCCCA 2156
DB 1901 CTGAGGTCAGAGTTCAAGACCAAGCCCTGGCCCAACATGTTGAACCCCA 1948

RESULT 66
US-09-154-602-6
Sequence 6, Application US/09154602
Patent No. 6300472
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Puri
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,602
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,901
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-154-602-6

Query Match 1.8%; Score 48; DB 3; Length 2713;
Best Local Similarity 100.0%; Pred. No. 3.9e-11;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAAGACTTCAAGACCAAGCTGGCCCAACATGTTGAAACCCCA 2156
|||||
DB 1901 CTGAGGTCAAGACTTCAAGACCAAGCTGGCCCAACATGTTGAAACCCCA 1948

RESULT 67
US-09-054-272-41/C
Sequence 41, Application US/09054272
Patent No. 6692909
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Daley, George Q.
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Rozen, Steven G.
TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,272
FILING DATE: 01-Apr-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH198-05
TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 26928 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-054-272-41

Query Match 1.8%; Score 48; DB 4; Length 26928;
Best Local Similarity 100.0%; Pred. No. 3.5e-11;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 GAGTCAAGACTTCAAGACCAAGCTGGCCCAACATGTTGAAACCCCATC 2158
|||||
DB 18730 GAGTCAAGACTTCAAGACCAAGCTGGCCCAACATGTTGAAACCCCATC 18683

RESULT 68
US-09-009-913-1/C
Sequence 1, Application US/09009913
Patent No. 6087485

GENERAL INFORMATION:
APPLICANT: Axy's Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-4P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 72928 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-009-913-1

Query Match 1.8%; Score 48; DB 3; Length 72928;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2120 AGTCAAGACCAAGCTGGCCCAACATGTTGAAACCCCATCTACTATAA 2167
|||||
DB 55445 AGTCAAGACCAAGCTGGCCCAACATGTTGAAACCCCATCTACTATAA 55398

RESULT 69

US-09-792-616-1
; Sequence 1, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: Pxe International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; FILE REFERENCE: Pxe-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 107820
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "n" can be an A or a T or a G or a C
US-09-792-616-1

Query Match 1.8%; Score 48; DB 4; Length 107820;
Best Local Similarity 100.0%; Pred. No. 3,3e-11;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2120 AGTTCAAGACCAGCTGCGCAACATGTGAAACCCCATCTCTACTATAA 2167
DB 60456 AGTTCAAGACCAGCTGCGCAACATGTGAAACCCCATCTCTACTATAA 60503

RESULT 70

US-10-148-806-3
; Sequence 3, Application US/10148806
; Patent No. 6762042
; GENERAL INFORMATION:
; APPLICANT: Bai, Chang
; APPLICANT: Metzger, Michael
; APPLICANT: Liu, Xiaomei
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
; FILE REFERENCE: 20585P
; CURRENT APPLICATION NUMBER: US/10/148,806
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US00/33065
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: 60/169,970
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 114793
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-148-806-3

Query Match 1.8%; Score 48; DB 4; Length 114793;
Best Local Similarity 100.0%; Pred. No. 3,3e-11;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2056 GTGGCTCACACCTGTATCCAGACATTTGGAGAGCCCAAGTGGGTGG 2103
DB 106838 GTGGCTCACACCTGTATCCAGACATTTGGAGAGCCCAAGTGGGTGG 106885

RESULT 71

US-09-513-999C-17885/C
; Sequence 7, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 17885

LENGTH: 274

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 146..

; OTHER INFORMATION: w=a or t

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 215

; OTHER INFORMATION: s=g or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 222

; OTHER INFORMATION: y=c or t

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 224

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 240

; OTHER INFORMATION: k=g or t

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 248

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 254

; OTHER INFORMATION: k=g or t

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 259

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 261

; OTHER INFORMATION: s=g or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 264

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 264

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 264

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 264

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 264

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 264

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 264

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 264

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 264

; OTHER INFORMATION: m=a or c

RESULT 72

US-08-849-701-7
; Sequence 7, Application US/08849701
; Patent No. 5922544
; GENERAL INFORMATION:
; APPLICANT: Miyai, Kiyoshi
; APPLICANT: Naitoh, Teutomu

Query Match 1.7%; Score 47; DB 4; Length 274;
Best Local Similarity 100.0%; Pred. No. 1,2e-10;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGTCAGGAGTTTCAGACGAGCTGGCCCAATGCGAAACCC 2155
DB 208 CTGAGTCAGGAGTTTCAGACGAGCTGGCCCAATGCGAAACCC 162

```

? APPLICANT: Yonekawa, Toshihiro
? TITLE OF INVENTION: Method of Cell Detection
? NUMBER OF SEQUENCES: 12
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Knobbe, Martens, Olson & Bear
? STREET: 620 Newport Center Drive 16th Floor
? CITY: Newport Beach
? STATE: CA
? COUNTRY: U.S.A.
? ZIP: 92660
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq Version 1.5
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/849,701
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/JP95/02734
? FILING DATE: 27-DEC-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: Altman, Daniel E
? REGISTRATION NUMBER: 34,115
? REFERENCE/DOCKET NUMBER: EIKEN1.001APC
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 714-760-0404
? TELEFAX: 714-760-9502
? TELEX:
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 280 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? CLONE: Alt sequence BUR11
? US-08-849-701-7

Query Match 1.7%; Score 47; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAAGAGTTCAAGACGAGCTGGCCACATGTAAGAAACCC 2155
DB 44 CTGAGGTCAAGAGTTCAAGACGAGCTGGCCACATGTAAGAAACCC 90

RESULT 73
US-08-133-629-8
? Sequence 8, Application US/08133629
? Patent No. 5597694
? GENERAL INFORMATION:
? APPLICANT: Munroe, David J.
? APPLICANT: Houseman, David E.
? TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
? STREET: 600 Atlantic Avenue
? CITY: Boston
? STATE: Massachusetts
? COUNTRY: United States of America
? ZIP: 02210
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/133,629
? FILING DATE: 07-OCT-1993
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? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Greer, Helen
? REGISTRATION NUMBER: 36,816
? REFERENCE/DOCKET NUMBER: M0828/7001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617-720-3500
? TELEFAX: 617-720-2441
? TELEX: 92-1742 EZEKTEL
? INFORMATION FOR SEQ ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 282 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? US-08-133-629-8

Query Match 1.7%; Score 47; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAAGAGTTCAAGACGAGCTGGCCACATGTAAGAAACCC 2155
DB 65 CTGAGGTCAAGAGTTCAAGACGAGCTGGCCACATGTAAGAAACCC 111

RESULT 74
US-08-579-445-26
? Sequence 26, Application US/08579445
? Patent No. 6566053
? GENERAL INFORMATION:
? APPLICANT: Perucho, Manuel
? APPLICANT: Peinado, Miguel A.
? APPLICANT: Ionov, Yuri
? APPLICANT: Malkhosyan, Sergei
? TITLE OF INVENTION: Identification of Neoplasms by Detection
? NUMBER OF SEQUENCES: 27
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Knobbe, Martens, Olson & Bear
? STREET: 620 Newport Center Drive, Sixteenth Floor
? CITY: Newport Beach
? STATE: CA
? COUNTRY: U.S.A.
? ZIP: 92660
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/579,445
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/152,484
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Kirkpatrick, Anita M.
? REGISTRATION NUMBER: 32,617
? REFERENCE/DOCKET NUMBER: STRATAG.009A
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (619) 235-8550
? TELEFAX: (619) 235-0176
? INFORMATION FOR SEQ ID NO: 26:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 283 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
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US-08-579-445-26

Query Match

Best Local Similarity 1.7%; Score 47; DB 4; Length 283;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAGGAGTTCAAGACCAAGCTGGCCACATGCTGTAACCCC 2155
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 65 CTGAGGTCAGGAGTTCAAGACCAAGCTGGCCACATGCTGTAACCCC 111

RESULT 75

US-09-513-999C-27220/c
 ; Sequence 27220, Application US/09513999C
 ; Patent No. 6783961
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J. B.
 ; APPLICANT: Duclert, A.
 ; APPLICANT: Giordano, J. Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; Patent No. 6783961
 ; FILE REFERENCE: 59.US2.REG
 ; CURRENT APPLICATION NUMBER: US/09/513,999C
 ; CURRENT FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/122,487
 ; PRIOR FILING DATE: 1999-02-26
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patent.Pm
 ; SEQ ID NO 27220
 ; LENGTH: 330
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 128
 ; OTHER INFORMATION: r=a or g
 US-09-513-999C-27220

Query Match

Best Local Similarity 1.7%; Score 47; DB 4; Length 330;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CTGAGGTCAGGAGTTCAAGACCAAGCTGGCCACATGCTGTAACCCC 2155
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 262 CTGAGGTCAGGAGTTCAAGACCAAGCTGGCCACATGCTGTAACCCC 216

Search completed: October 28, 2004, 19:22:26
 Job time : 238 secs

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